

Figure 1. Muscle cramping of the Cra1 mouse.



Cra1/+

+/+

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Figure 2. Increased ambulatory activity of
Cra1 mice during the night.

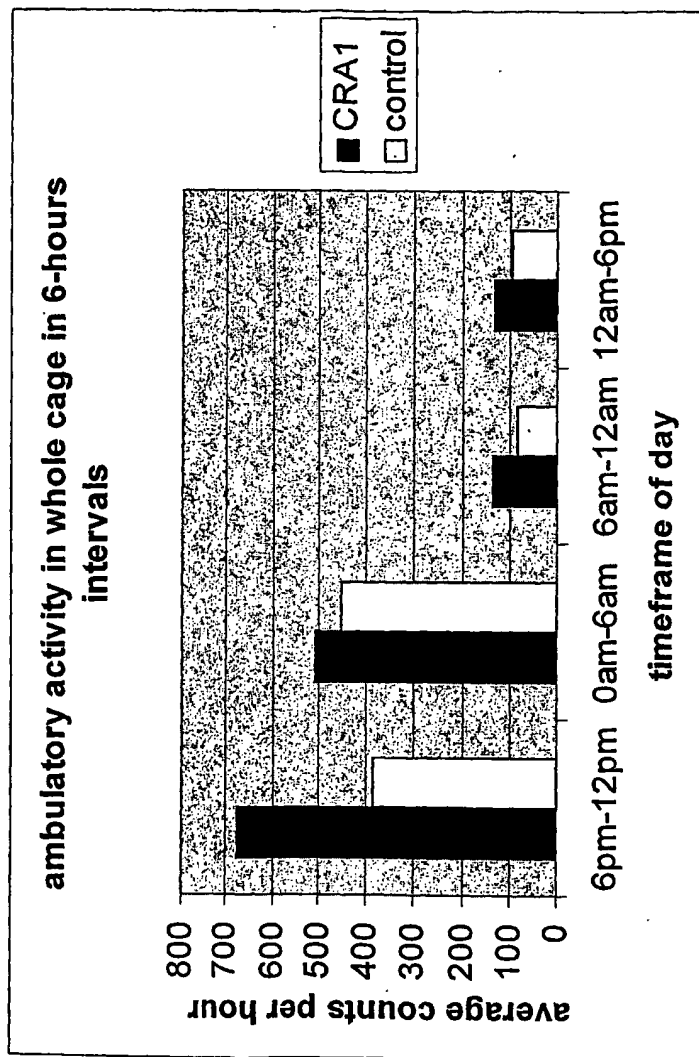
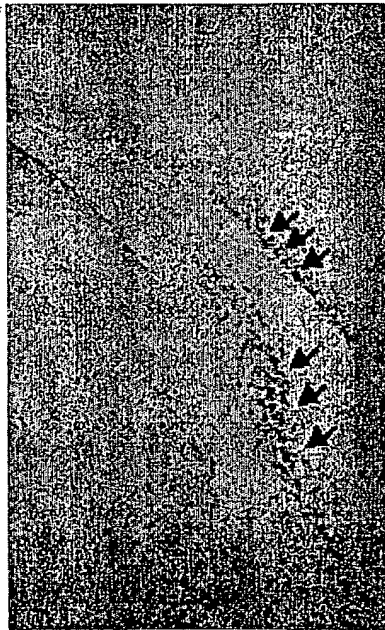


Figure 3. Reduced muscle endurance of *Cral* mice.

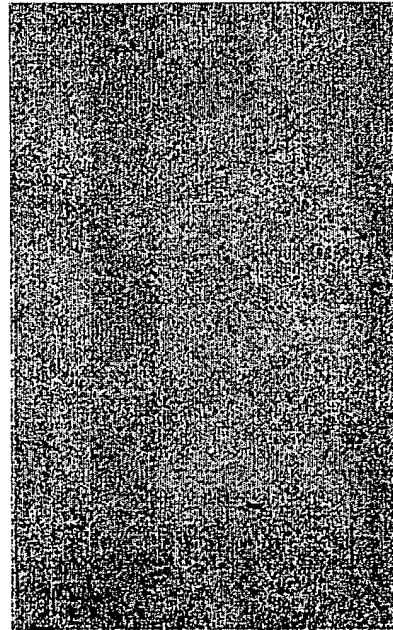
<u>Mouse #</u>	<u>Sex</u>	<u>Genotype</u>	<u>Latency to Fall [in seconds]</u>
1	female	+/+	810
2	male	+/+	280
3	male	+/+	845
4	female	<i>Cral</i> /+	110
5	female	<i>Cral</i> /+	15
6	female	<i>Cral</i> /+	35
7	male	<i>Cral</i> /+	14
8	male	<i>Cral</i> /+	20
9	male	<i>Cral</i> /+	20

Figure 4. Excitatory neuronal damage in the hippocampus of the *Cra1* mouse.

Cra1^{+/+}

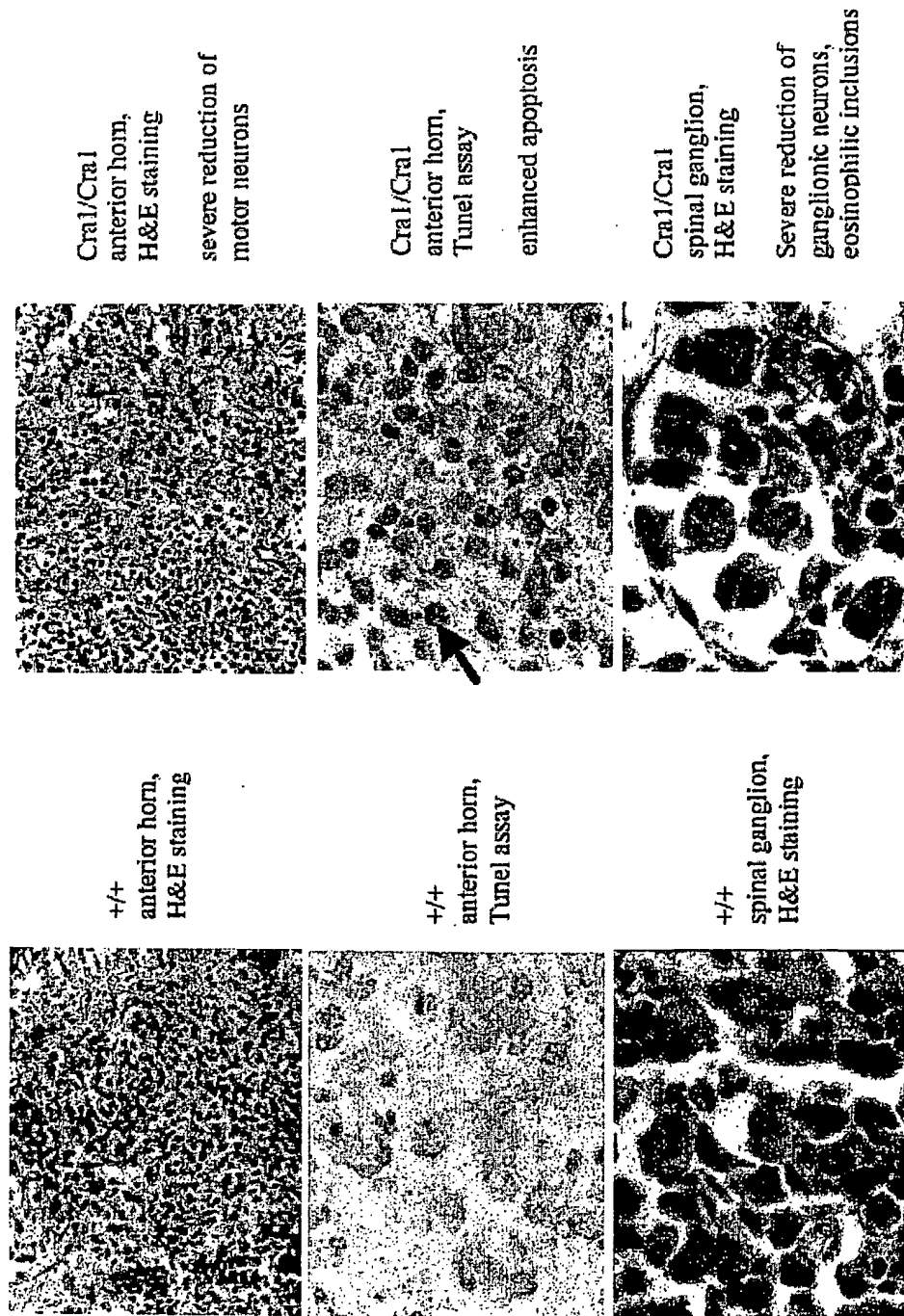


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Figure 5. Neurodegeneration in the anterior horns of the spinal cord and the dorsal root ganglia of homozygous Cra1 embryos.



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Figure 5.2: Progressive impairment of muscle function and motor coordination is associated with decreasing numbers of a-motor neurons and altered composition of muscle fibre types.

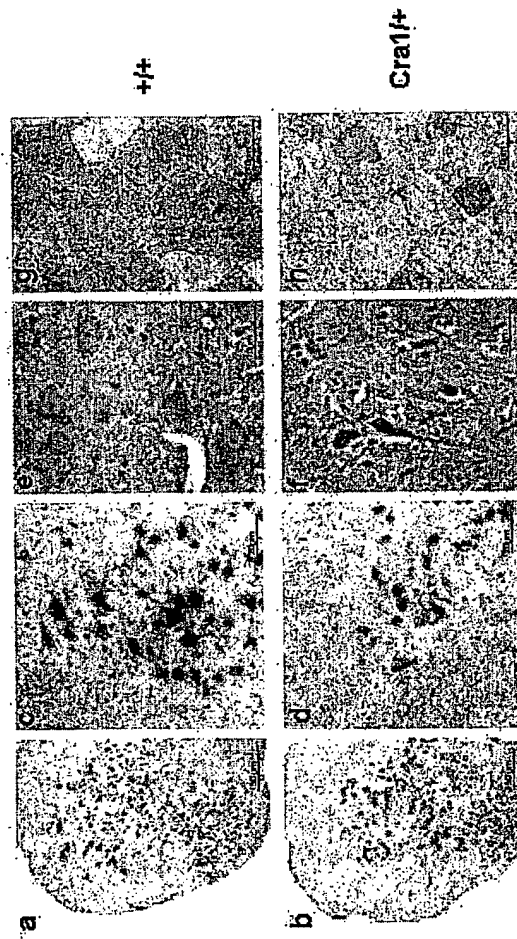
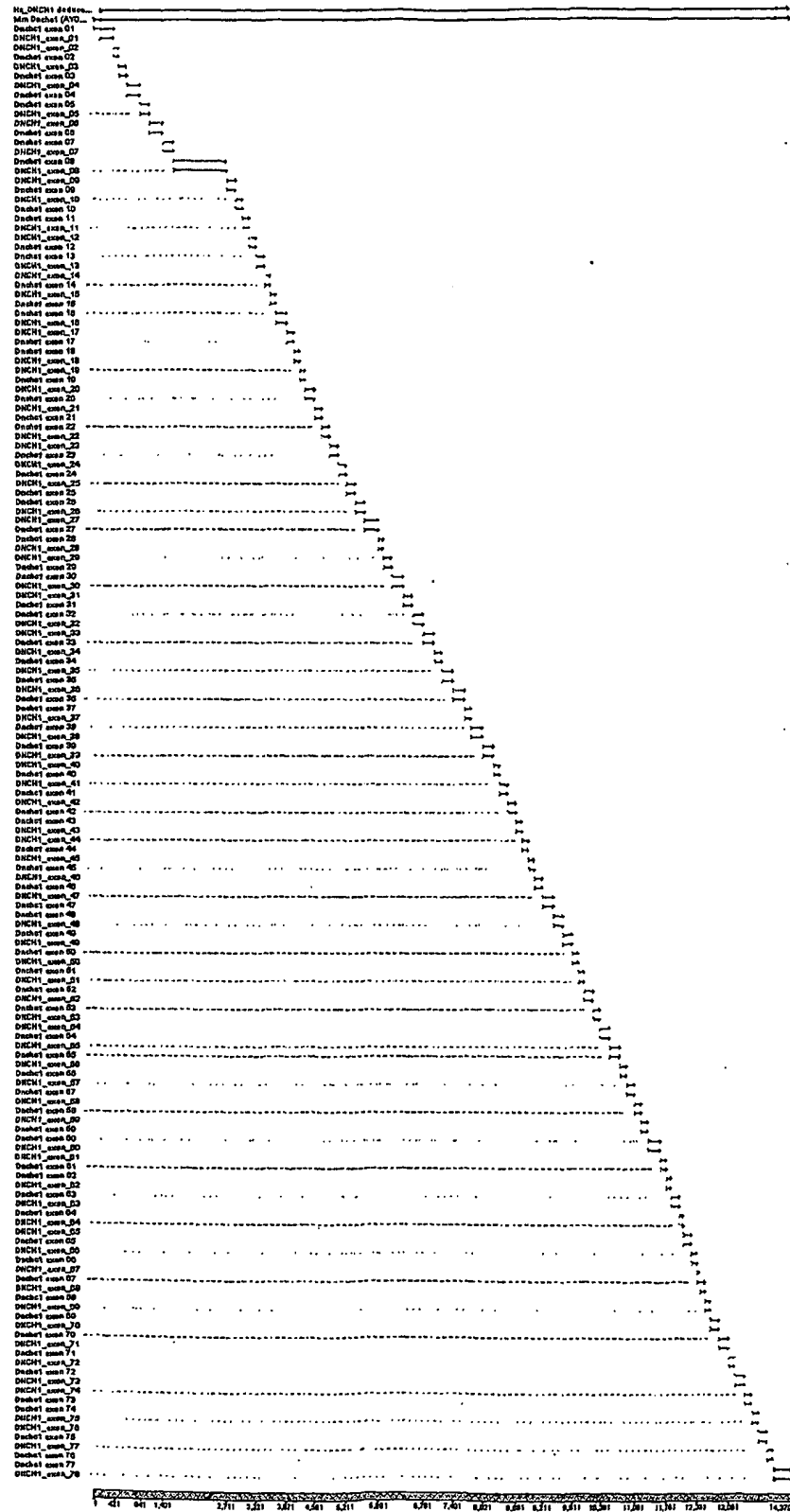


Figure 6. Transcriptionally deregulated genes in the brain of homozygous Cra1 embryos.

Gene symbol	Gene description	Deregulation	Biological significance
Rasgrp2	RAS, guanyl releasing protein 2	Up	Brain-enriched guanine nucleotide exchange factor, is stimulated by calcium and glycylglycylglycyl and activates small GTPases (e.g. Ras); expressed in the striatal projection neurons (cf. Toki et al. 2001, J Comp Neurol 437, 398-407)
Vdac2	voltage-dependent anion channel 2	Down	Voltage dependent anion channel of the outer mitochondrial membrane; controls the permeability of outer mitochondrial membrane for anions (eg ATP); probably part of the permeability transition pore (involved in apoptosis regulation); KO mouse displays immobile sperms and infertility (axonal defects of the sperms) as well as deficits in long and short term synaptic plasticity, fear conditioning and spatial learning (cf. Wajsborg et al. 2002, J Biol Chem 277, 18891-18897).
Ttc3	tetratricopeptide repeat domain	Down	Domain on transcription factors that allows them to bind to an acceptor site on the ubiquitous hsp90 protein; some of these transcription factors bind to cytoplasmic dynein; the complex of the hsp90-GR (glucocorticoid receptor)-FKBP-52 is targeted to the nucleus by binding of the latter to dynein (cf. Harrell et al. 2002, 41, 5581-5587)
Rab6	RAB6, member RAS oncogene family	Down	Rab proteins are molecular switches or timers regulating the transport of vesicles between compartments of the cell (eg golgi and ER); they impart the recruitment of dynein to the intracellular vesicles which have to be transported (cf. Smythe 2002, Mol. Cell 9, 205-206; Seabra et al 2002, Trends Mol Med 8, 23-30)
Rab2	RAB2, member RAS oncogene family	Down	Rab proteins are molecular switches or timers regulating the transport of vesicles between compartments of the cell (eg golgi and ER); they impart the recruitment of dynein to the intracellular vesicles which have to be transported (cf. Smythe 2002, Mol. Cell 9, 205-206; Seabra et al 2002, Trends Mol Med 8, 23-30)
Pak3	p21 (CDKN1A)-activated kinase 3	Down	PAK proteins (p21 activating kinases) are downstream effectors that link Rho-GTPases to the actin cytoskeleton and to MAP kinase cascades, including the c-Jun amino-terminal kinase (JNK) and p38. Recently it has been shown, that the presence of mutations in Pak3 is associated with X-linked non-specific mental retardation (Bjerve et al. 2000, Am J Med Genet 93, 294-298)
Mark3	MAP/microtubule affinity-regulating kinase 3	Down	Belongs to a family of kinases which phosphorylates microtubule-associated proteins (e.g. tau) and trigger microtubule disruption (cf. Dreyer et al 1997, Cell 89, 297-308); tau is hyperphosphorylated in several neurodegenerative diseases including Alzheimer's disease (cf. Schneider et al. 1999, Biochemistry 38, 3549-3558)
Kir3b	kinase family member 3b	Down	Component of the adenosine triphosphatase motor kinesin (Yamazaki et al 1995, J Cell Biol 130, 1387-1399)
Drg1	developmentally regulated GTP binding protein 1	Down	DRG is a developmentally regulated GTP-binding protein from the central nervous system of mouse (Li and Tu, 2000, Biochim Biophys Acta 1491, 196-204)
Clcn3	chloride channel 3	Down	Clc3 chloride channel is expressed in nervous tissue; the KO mouse displays blindness, motor coordination deficit, spontaneous hyperexcitability, retinal and hippocampal degeneration; the observed phenotype seems to be due to an accumulation of the neuronal cargo lipofuscin
Ecan	ecavican	Down	Ecavican is an extracellular matrix molecule (proteoglycan) which is overexpressed in human gliomas (Jaworski et al 1996, Cancer Research 56, 2283-2298). It seems to inhibit neurite outgrowth thereby contributing to axon guidance in development and regenerative processes (cf. Peller et al. 2001, Restor Neurol Neurosci 19, 159-167)

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Figure 7. Exon Structure Comparison between the Human DNCH1 and the Mouse Dnchc1 Genes.



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Figure 8. Comparison of mouse and human dynein heavy chain 1 exon numbers and exon lengths.

Exon No.	Mm Dnchc1 (bp)	Hs DNCH1 (bp)	Exon No.	Mm Dnchc1 (bp)	Hs DNCH1 (bp)
1	250	256	40	122	122
2	88	88	41	166	166
3	174	174	42	164	164
4	256	256	43	130	130
5	187	187	44	134	134
6	272	272	45	115	115
7	228	228	46	162	162
8	1078	1078	47	215	215
9	180	180	48	205	205
10	150	150	49	174	174
11	147	147	50	120	120
12	141	141	51	121	121
13	177	177	52	196	196
14	111	111	53	118	118
15	120	120	54	216	216
16	240	240	55	213	213
17	156	156	56	128	128
18	114	114	57	154	154
19	111	111	58	147	147
20	210	210	59	151	151
21	147	147	60	254	254
22	167	167	61	135	135
23	174	174	62	95	95
24	166	166	63	175	175
25	189	189	64	76	76
26	195	195	65	161	161
27	283	283	66	112	112
28	101	101	67	185	61
29	160	160	68	114	124
30	244	244	69	171	114
31	184	184	70	218	171
32	213	213	71	104	218
33	239	239	72	212	104
34	157	157	73	154	212
35	228	228	74	143	154
36	231	231	75	169	143
37	141	141	76	128	169
38	234	234	77	129	128
39	207	207	78		129

Figure 9. Amino Acid Alignment of Human DNCH1 and Mouse Dnchc1 Proteins.

Hs_DNCH1	1	KSEPGGGGEGDSAGLEVSAVQNVADVSLQKHRLKPLVLLLEDGGEPAALAEAEKSALEQMRKFLSDPQVHTVIVVERSTLKEDVGDGEEKEKEFTS
Mm_Dnchc1	1	KSEPGGG...EDGSAGLEVSAVQNVADVA/LQKHRLKPLVLLLEDGGEPAALAEAEKSALEQMRKFLSDPQVHTVIVVERSTLKEDVGDGEEKEKEFTS
Hs_DNCH1	101	YMINLDIYGVKSNSLAFIKETPVLDADKPVSQSLRVLTLSSEDSPYETLHSTFISNAVAPFFKSYIRESKADRDGDKMAPSVVEKKTAELENGLLHLQQNI
Mm_Dnchc1	99	YMINLDIYGVKSNSLAFIKETPVLDADKPVSQSLRVLTLSSEDSPYETLHSTFISNAVAPFFKSYIRESKADRDGDKMAPSVVEKKTAELENGLLHLQQNI
Hs_DNCH1	201	EIPEISLPIHEHITTHVAKQCYERGEKPKVTDGDKVEDPTEINQOSGVNRWIREIQKVTIKLDRDPASGTALQEI SFWHLERAIYRQEKRESPEVLLT
Mm_Dnchc1	199	EIPEISLPIHEHITTHVAKQCYERGEKPKVTDGDKVEDPTEINQOSGVNRWIREIQKVTIKLDRDPASGTALQEI SFWHLERAIYRQEKRESPEVLLT
Hs_DNCH1	301	LDILKIKGRPHATVSDFTDTGLKQALETVNDYNPLMKDFPLNDLLSATLQKIRALVAIETHLRKIRNTKYPIORALRLVEAISRDLSOLLKVLGTRK
Mm_Dnchc1	299	LDILKIKGRPHATVSDFTDTGLKQALETVNDYNPLMKDFPLNDLLSATLQKIRALVAIETHLRKIRNTKYPIORALRLVEAISRDLSOLLKVLGTRK
Hs_DNCH1	401	LHVAYEEFEKVMVACFEVFQTDDEYEKQLVLRDILVKKRKEENLWVRINPAHRKLOARLDQGRKERRQHEQOLRAVIVRLRQVATAVQOQNGEVP
Mm_Dnchc1	399	LHVAYEEFEKVMVACFEVFQTDDEYEKQLVLRDILVKKRKEENLWVRINPAHRKLOARLDQGRKERRQHEQOLRAVIVRLRQVATAVQOQNGEVP
Hs_DNCH1	501	EPQDMKVAEVLFDADANALIEEVNLAYENKREVLDGLVSKEGTEAWEAAMKRYDERIDRVETRIITARLDQLGTAKNAMEMERIESRFALEVRPHIRGA
Mm_Dnchc1	499	EPQDMKVAEVLFDADANALIEEVNLAYENKREVLDGLVSKEGTEAWEAAMKRYDERIDRVETRIITARLDQLGTAKNAMEMERIESRFALEVRPHIRGA
Hs_DNCH1	601	IREYQTLQIQRVKDDIESLHDKFKVQVPOSQACRMSHVRLDLPVSGSIIWAKQIDRQLTAYMKRVEDVLGKRWENHVEGQKLKQDGDSPRMKINTQEIIFD
Mm_Dnchc1	599	IREYQTLQIQRVKDDIESLHDKFKVQVPOSQACRMSHVRLDLPVSGSIIWAKQIDRQLTAYMKRVEDVLGKRWENHVEGQKLKQDGDSPRMKINTQEIIFD
Hs_DNCH1	701	QWARKVQORNGLVSGRIFTTIESTRVGRGTGNVLKLVNFELPEITLSKEVRNLKWLGRFVPIAIVNKAHQANQLYPPFAISLIESVRYTERTCEKVEERNY
Mm_Dnchc1	699	QWARKVQORNGLVSGRIFTTIESTRVGRGTGNVLKLVNFELPEITLSKEVRNLKWLGRFVPIAIVNKAHQANQLYPPFAISLIESVRYTERTCEKVEERNY
Hs_DNCH1	801	ISLLVAGLKKREVOALLAEGTALVWESYKLDIPYQRLAETVFNFOEKVDLLIIIEKIDLEVRSLCTCYDHKTFSEILNRVQKAVDDDLRLHSYSLPIRV
Mm_Dnchc1	799	ISLLVAGLKKREVOALLAEGTALVWESYKLDIPYQRLAETVFNFOEKVDLLIIIEKIDLEVRSLCTCYDHKTFSEILNRVQKAVDDDLRLHSYSLPIRV
Hs_DNCH1	901	NKLDMEIERILGVRLQAGLRATQVLLGQAEKAEVDMDTDAPQVSHKPGGEPKIKWVHELRIITNOVIYINLPPITEECRYKLYQEMFAKMWVLSLPIRQ
Mm_Dnchc1	899	NKLDMEIERILGVRLQAGLRATQVLLGQAEKAEVDMDTDAPQVSHKPGGEPKIKWVHELRIITNOVIYINLPPITEECRYKLYQEMFAKMWVLSLPIRQ
Hs_DNCH1	1001	SQRVQGVHYVELTEEEKFYRNALTRMPDGPVVALEESYSANVGIYVEVEQYKVMVQLQVCLMDQAEHIYNNRIGEDLNKQALLVQIRKARGTFDNAETKK
Mm_Dnchc1	999	SQRVQGVHYVELTEEEKFYRNALTRMPDGPVVALEESYSANVGIYVEVEQYKVMVQLQVCLMDQAEHIYNNRIGEDLNKQALLVQIRKARGTFDNAETKK
Hs_DNCH1	1101	EFGPVVDYDKVQSKVNLKYDSHHEKVLSEKQGLGNNMTFFHSQISKSRQELQHSVDFTASTDAVFTFYVQS/LKRIKQEFQVQVLYRNGQRLLEKO
Mm_Dnchc1	1099	EFGPVVDYDKVQSKVNLKYDSHHEKVLSEKQGLGNNMTFFHSQISKSRQELQHSVDFTASTDAVFTFYVQS/LKRIKQEFQVQVLYRNGQRLLEKO
Hs_DNCH1	1201	RFQPPPSWLYIDNIEGEGGAFNDIMRRKDSAIQQVAVLQMKIVQEDRAVESRTDLDLTDHEKTKPTGNLRPEALQALTIYEGKFGRLKDDREKCAKA
Mm_Dnchc1	1199	RFQPPPSWLYIDNIEGEGGAFNDIMRRKDSAIQQVAVLQMKIVQEDRAVESRTDLDLTDHEKTKPTGNLRPEALQALTIYEGKFGRLKDDREKCAKA

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(Figure 9 continued)

Hs_DNCH1 1301 KDALEITDGLSGSERVQVALEELQDLKNGWSELKSWEQIDQMKQEPWVSQPRKLRQNDLFLINQKLSFARLRQVASYEFVORLLKGYMKINMLV
 Mm_Dnchc1 1299 KDALEITDGLSGSERVQVALEELQDLKNGWSELKSWEQIDQMKQEPWVSQPRKLRQNDLFLINQKLSFARLRQVASYEFVORLLKGYMKINMLV
 Hs_DNCH1 1401 IEKSEALKDRHWKQIMKRLHVNWVSEITLGOIMDVQDKNEATIKDVLVAQSGMALEEFKQIREVNTVYELDLVNYQNKCRITRGWDDLEFNKVKKEH
 Mm_Dnchc1 1399 IEKSEALKDRHWKQIMKRLHVNWVSEITLGOIMDVQDKNEATIKDVLVAQSGMALEEFKQIREVNTVYELDLVNYQNKCRITRGWDDLEFNKVKKEH
 Hs_DNCH1 1501 INSVAMKLSPPYKVFEDALSWEDKLRIMALFDWVIDVQRWVYLEGITFTGSADIKHLLPVETQFOSISTEFLALMKKSKSPLMVDVNLQGVQORS
 Mm_Dnchc1 1499 INSVAMKLSPPYKVFEDALSWEDKLRIMALFDWVIDVQRWVYLEGITFTGSADIKHLLPVETQFOSISTEFLALMKKSKSPLMVDVNLQGVQORS
 Hs_DNCH1 1601 LERLADLLGKIQKALGEYLERSSFPRTFYFGDEDELLEIGNSKRVAKLRHFKFAGVASSIILNEONSVLGTSRREGEVMEFTVPSITTEHPKINE
 Mm_Dnchc1 1599 LERLADLLGKIQKALGEYLERSSFPRTFYFGDEDELLEIGNSKRVAKLRHFKFAGVASSIILNEONSVLGTSRREGEVMEFTVPSITTEHPKINE
 Hs_DNCH1 1701 MTLVEKEMRVTLAKLLAESVTEVEIFGKATSIDENTVYITWIDKYQAQVWLSAQIAEENVENALSMGGGGDYPLQSVLSNVVETLVNLADSVLINEQ
 Mm_Dnchc1 1699 MTLVEKEMRVTLAKLLAESVTEVEIFGKATSIDENTVYITWIDKYQAQVWLSAQIAEENVENALSMGGGGDYPLQSVLSNVVETLVNLADSVLINEQ
 Hs_DNCH1 1801 PPLRRKLEHLITELVHORDVTRSLIKSKI DNKAKSEFMSQHRFYEDPKQTDVLOQLSIQMANAKFNVEEYIGVQDKLVQVTELTDRCYLTMTQALEARL
 Mm_Dnchc1 1799 PPLRRKLEHLITELVHORDVTRSLIKSKI DNKAKSEFMSQHRFYEDPKQTDVLOQLSIQMANAKFNVEEYIGVQDKLVQVTELTDRCYLTMTQALEARL
 Hs_DNCH1 1901 SGSPGPACTGKTESVKALGHQGRFVLVFNCDENFDQAGRIIFVGLQGVANGCFDEFNRLEERMSAVSQVQCIQDALREHNSPNVDKTSAPITCE
 Mm_Dnchc1 1899 SGSPGPACTGKTESVKALGHQGRFVLVFNCDENFDQAGRIIFVGLQGVANGCFDEFNRLEERMSAVSQVQCIQDALREHNSPNVDKTSAPITCE
 Hs_DNCH1 2001 LANKQVKSPOMAIFITMNPYAGKSNLPDNLKLFRLSIAMTKPQRLTAQVMLYSQGRFAEVLANKIUPPFKLCDEQLSSQSHYDFGLRALKSLVLSA
 Mm_Dnchc1 1999 LANKQVKSPOMAIFITMNPYAGKSNLPDNLKLFRLSIAMTKPQRLTAQVMLYSQGRFAEVLANKIUPPFKLCDEQLSSQSHYDFGLRALKSLVLSA
 Hs_DNCH1 2101 GNVRERIQKIKREKEGEAVDEGEIAENLPEQELLIQSVCTETVPKLVAEADIPLPLSLSDVPFGVQYHRGEMTALREELKKVCQENYLTVDGDEEVG
 Mm_Dnchc1 2099 GNVRERIQKIKREKEGEAVDEGEIAENLPEQELLIQSVCTETVPKLVAEADIPLPLSLSDVPFGVQYHRGEMTALREELKKVCQENYLTVDGDEEVG
 Hs_DNCH1 2201 GAWVEKVLQLYQITQINHGILMWGPGSGKSNAMRVLLKALERLEGVEGVAHIIDPKAISKDHLGTLDPNPREMTDGLFTHVLKLIISVRGELQKROH
 Mm_Dnchc1 2199 GAWVEKVLQLYQITQINHGILMWGPGSGKSNAMRVLLKALERLEGVEGVAHIIDPKAISKDHLGTLDPNPREMTDGLFTHVLKLIISVRGELQKROH
 Hs_DNCH1 2301 LVFGDGDVDPWVENLNSVLDNKKLTLTPNGERLSLPPNVRIMFVQDILKYATLATVSRCCGWVWFSEDLVSTDMIENNFLARLSIPLDEGEDEAQRRRKG
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 Hs_DNCH1 2501 SLSDSRKMKRAELGEYIRRIITVPLTPAPNPIIDYEVSISEGSWSPQAKVPOLEVETHKVAADVVVPTLDVVRHEALLYTWLAHEKPLVLCGPPGSG
 Mm_Dnchc1 2499 SLSDSRKMKRAELGEYIRRIITVPLTPAPNPIIDYEVSISEGSWSPQAKVPOLEVETHKVAADVVVPTLDVVRHEALLYTWLAHEKPLVLCGPPGSG
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 Mm_Dnchc1 2599 KTWTLFSAALRALPDMEVUGLNFSSATTEPELLKTEDHYCEYRRTPNGVWLPAPVOLGKWLVLFCDEINLPDMDKYGTQVISEITROMVEHGFRTSDQW
 Hs_DNCH1 2701 VKLRIQFVGACNPPTDGRKPLSHRFLRHVPVYVDYVPGASITQIYGTENRAMRLIPLSIRTYAEPLTAMVEFTMSQERFTQDQPHYIYSPREMT
 Mm_Dnchc1 2699 VKLRIQFVGACNPPTDGRKPLSHRFLRHVPVYVDYVPGASITQIYGTENRAMRLIPLSIRTYAEPLTAMVEFTMSQERFTQDQPHYIYSPREMT
 Hs_DNCH1 2801 RWRGIFEARPLETLPVEGLIRITWAHEALRALFODRLVEDEERRWTDENIIVALKHFPNIDHEKAMSRPILYSNMLSKDYIPVDQETLRDYVKARLKV
 Mm_Dnchc1 2799 RWRGIFEARPLETLPVEGLIRITWAHEALRALFODRLVEDEERRWTDENIIVALKHFPNIDHEKAMSRPILYSNMLSKDYIPVDQETLRDYVKARLKV

(Figure 9 continued)

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Hs_DNCH1 2901 YEEELDVPLVLFNEVLDPVLRIDRIFRQPOGHLLILIGVSGAGRTTLRSFVAMNGLSVYQIKVHRKYTGEDFEDLRTVLRSGCKNEKIAFINDESNNL
 Mm_Dnchc1 2899 YEEELDVPLVLFNEVLDPVLRIDRIFRQPOGHLLILIGVSGAGRTTLRSFVAMNGLSVYQIKVHRKYTGEDFEDLRTVLRSGCKNEKIAFINDESNNL
 Hs_DNCH1 3001 DSGFLERANWLLANGVEVPLGPEGDEYATLMTQCKEGAKQEGMLDSHEELKYKWTQSQUIRNLHVWFTWNPSSSEGLKDRATSPALFNRCVLNFWGDMSTE
 Mm_Dnchc1 2999 DSGFLERANWLLANGVEVPLGPEGDEYATLMTQCKEGAKQEGMLDSHEELKYKWTQSQUIRNLHVWFTWNPSSSEGLKDRATSPALFNRCVLNFWGDMSTE
 Hs_DNCH1 3101 ALXOVGREFTSKMOLKPNXIVPDYMPVVDKLPQPPHREAIWNSCVFVHQTILQANARLAKRGGRMTATPRHYLDFINHYANLFEKRSSELEEQMH
 Mm_Dnchc1 3099 ALXOVGREFTSKMOLKPNXIVPDYMPVVDKLPQPPHREAIWNSCVFVHQTILQANARLAKRGGRMTATPRHYLDFINHYANLFEKRSSELEEQMH
 Hs_DNCH1 3201 UNVGLRKIKETVDOVEELRRDLRIKSOELEVNAAANDKLKVVQDOEAKKVMQSOETQEOHLHQOEVTAADKMSVKEDIDKVEPAVIEAQNAAVSKIK
 Mm_Dnchc1 3199 UNVGLRKIKETVDOVEELRRDLRIKSOELEVNAAANDKLKVVQDOEAKKVMQSOETQEOHLHQOEVTAADKMSVKEDIDKVEPAVIEAQNAAVSKIK
 Hs_DNCH1 3301 KOHLVEVRSNANPPAAVKLALLESICLLGSETTDMKQIIRSIINRENFPTIVNPSABEISDAIREKKKNVMSNPSYNYEIVNRSALACGPMVWVAIAQL
 Mm_Dnchc1 3299 KOHLVEVRSNANPPAAVKLALLESICLLGSETTDMKQIIRSIINRENFPTIVNPSABEISDAIREKKKNVMSNPSYNYEIVNRSALACGPMVWVAIAQL
 Hs_DNCH1 3401 AYADMLKRVPLRNELOKLEDDAKQKANEVEQNIROLEASITARYKEEYAVLISAQAIKADLAAVEAKVNRSTALLKLSABERERWEKTSSETTKQOM
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 Hs_DNCH1 3501 STIAGDCLLSAAFIAYAGYFDQOMRQHLFTWSSHLLQOANIQRTDITARTYELSNADERLRWQASSIPADDLCCTENAIMLRFNRYPLIIDPSGOATEFI
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 Hs_DNCH1 3701 FTWTRSSLOSCLNEVILKAEKRPDVKERSDLLKLOGEFOLRLQLEKSLLOALNEVKGRIIIDDITITLENLAREAAEVTRKVEETDVAQOEVETVSQC
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 Hs_DNCH1 3801 YPLSTACSSIIYFTMESLQVHELYQYSLOFFLDIYHNVLYENPNLKGVDHTQRLSIITKDLFOVAFNRVARGMHQDHTFANILLARIKLKGTVGEBPT
 Mm_Dnchc1 3799 YPLSTACSSIIYFTMESLQVHELYQYSLOFFLDIYHNVLYENPNLKGVDHTQRLSIITKDLFOVAFNRVARGMHQDHTFANILLARIKLKGTVGEBPT
 Hs_DNCH1 3901 YDAEQHFILRGNEIVLSAGSTPFIQGLTVEQAEAVVRLSCLPAFKOLIAKQVQADEQEGWLDSSSPQOTVYILWSEETPATPIGOATHRLILLIOAFRDDR
 Mm_Dnchc1 3899 YDAEQHFILRGNEIVLSAGSTPFIQGLTVEQAEAVVRLSCLPAFKOLIAKQVQADEQEGWLDSSSPQOTVYILWSEETPATPIGOATHRLILLIOAFRDDR
 Hs_DNCH1 4001 LLAMAHMFVSTNLGSEFMSIMEQPLDLTHIVGTEVAPNTPVLMCSVPGYDASGHVEDLAEOQTOITSLAIGSAEGFNOADKANTAVKSGRAWMLKNVH
 Mm_Dnchc1 3999 LLAMAHMFVSTNLGSEFMSIMEQPLDLTHIVGTEVAPNTPVLMCSVPGYDASGHVEDLAEOQTOITSLAIGSAEGFNOADKANTAVKSGRAWMLKNVH
 Hs_DNCH1 4101 LAPGHLMOLEKRLHLSLOPHACFRLEFIMEINPKVPVNLIRAGSIFVFEPPPGVKNMLRFTSSIPVSRICKSPNERARLYELLAWFHAIIOERLRYAPLG
 Mm_Dnchc1 4099 LAPGHLMOLEKRLHLSLOPHACFRLEFIMEINPKVPVNLIRAGSIFVFEPPPGVKNMLRFTSSIPVSRICKSPNERARLYELLAWFHAIIOERLRYAPLG
 Hs_DNCH1 4201 HSKKYEFGESDLSRACDVTWLDLDTAKGRQMSIPDKIPASALKTIMAQSIVGGRVDNEEDQRLNLTFLERLFTTTSFDSSEFKLACKVDGKDIQMPDGI
 Mm_Dnchc1 4199 HSKKYEFGESDLSRACDVTWLDLDTAKGRQMSIPDKIPASALKTIMAQSIVGGRVDNEEDQRLNLTFLERLFTTTSFDSSEFKLACKVDGKDIQMPDGI
 Hs_DNCH1 4301 RREEVQWVELLPDQTPPSWGLPNNARVLLTQGVDMISRLNRQMLEDDEDLAYATEKERTDSTSDGRPAWMTLHTTASNWLHLIPQTLSHLKR
 Mm_Dnchc1 4299 RREEVQWVELLPDQTPPSWGLPNNARVLLTQGVDMISRLNRQMLEDDEDLAYATEKERTDSTSDGRPAWMTLHTTASNWLHLIPQTLSHLKR
 Hs_DNCH1 4401 TVENIKDPLFRFFEREVKGAKLLOOVRODLADVQVCEGKKTQNYLNTLINELVKGLIPRSWSHYTPAGTIVQWSDFSERIKOLQNISQAASGG
 Mm_Dnchc1 4399 TVENIKDPLFRFFEREVKGAKLLOOVRODLADVQVCEGKKTQNYLNTLINELVKGLIPRSWSHYTPAGTIVQWSDFSERIKOLQNISQAASGG

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(Figure 9 continued)

Hs_DNCH1	4501	AKELKNIHVCLGGLFVPEAYITATROYVAQANMSLEEICLEVNVITTSQATLDACSGVTGKLGQATCNNNKLSLSNAISTALPLTQLRWVKQNTEN
Mm_Dnchcl	4499	AKELKNIHVCLGGLFVPEAYITATROYVAQANMSLEEICLEVNVITTSQATLDACSGVTGKLGQATCSNNKLSLSNAISTALPLTQLRWVKQNTSAEK
Hs_DNCH1	4601	KASVVTLPVYLNFTRADLIFTVDFEITATKEDPRSFYERGVAVLCDE
Mm_Dnchcl	4599	KASVVTLPVYLNFTRADLIFTVDFEITATKEDPRSFYERGVAVLCDE

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Figure 10. Amino Acid Alignment of Human DNCH1, Mouse Dnchc1, and rat Dnchc1 Proteins –highly conserved amino acid residues.

Software used:

- MultAlin via <http://prodes.toulouse.inra.fr/multalin/multalin.html> [Corpet. F. (1988), Multiple sequence alignment with hierarchical clustering, Nucl. Acids Res., 16 (22), 10881-10890]
- BOXSHADE 3.21 via http://www.ch.embnet.org/software/BOX_form.html

Hs: Homo sapiens; deduced by homology
 Mm: Mus musculus; NP_084514
 Rn: Rattus norvegicus; NP_062099

Mm	1	MSPEGG...EDGSAGLEVS	AVQNVADV	LVQKHRLK	VLPLED	EGDAPAA	LEAALEKSA	LEQMKR	FLSD	QVHTVL	VERSTL	KEDV	DGDE	GEKE	EFIS																																											
Rn	1	MSPEGG...EDGSAGLEVS	AVQNVADV	LVQKHRLK	VLPLED	EGDAPAA	LEAALEKSA	LEQMKR	FLSD	QVHTVL	VERSTL	KEDV	DGDE	GEKE	EFIS																																											
Hs	1	MSPEGG...EDGSAGLEVS	AVQNVADV	LVQKHRLK	VLPLED	EGDAPAA	LEAALEKSA	LEQMKR	FLSD	QVHTVL	VERSTL	KEDV	DGDE	GEKE	EFIS																																											
Consensus	1	MSPEGG...EDGSAGLEVS	AVQNVADV	LVQKHRLK	VLPLED	EGDAPAA	LEAALEKSA	LEQMKR	FLSD	QVHTVL	VERSTL	KEDV	DGDE	GEKE	EFIS																																											
Mm	99	YNIIDIHGVK	NSLAFIK	RAPIV	LDAD	KPVSSQ	LRVLT	LSDDSP	YETL	HSFT	SNVAP	FFKSY	I	RESG	KADRDG	KNAPS	VEKKI	TAEL	ENG	LHL	QQNI																																					
Rn	99	YNIIDIHGVK	NSLAFIK	RAPIV	LDAD	KPVSSQ	LRVLT	LSDDSP	YETL	HSFT	SNVAP	FFKSY	I	RESG	KADRDG	KNAPS	VEKKI	TAEL	ENG	LHL	QQNI																																					
Hs	101	YNIIDIHGVK	NSLAFIK	RAPIV	LDAD	KPVSSQ	LRVLT	LSDDSP	YETL	HSFT	SNVAP	FFKSY	I	RESG	KADRDG	KNAPS	VEKKI	TAEL	ENG	LHL	QQNI																																					
Consensus	98	YNIIDIHGVK	NSLAFIK	RAPIV	LDAD	KPVSSQ	LRVLT	LSDDSP	YETL	HSFT	SNVAP	FFKSY	I	RESG	KADRDG	KNAPS	VEKKI	TAEL	ENG	LHL	QQNI																																					
Mm	199	EIPEISLP	IIITN	VAKQCY	ERGEK	PKVT	DGDK	VEDPT	FINQ	LQSG	VNWR	IRI	ETQ	KVTK	LDROP	PASG	TALQ	ETIS	F	WLN	LERAL	YRIQ	EKR	RES	PEV	LLT																																
Rn	199	EIPEISLP	IIITN	VAKQCY	ERGEK	PKVT	DGDK	VEDPT	FINQ	LQSG	VNWR	IRI	ETQ	KVTK	LDROP	PASG	TALQ	ETIS	F	WLN	LERAL	YRIQ	EKR	RES	PEV	LLT																																
Hs	201	EIPEISLP	IIITN	VAKQCY	ERGEK	PKVT	DGDK	VEDPT	FINQ	LQSG	VNWR	IRI	ETQ	KVTK	LDROP	PASG	TALQ	ETIS	F	WLN	LERAL	YRIQ	EKR	RES	PEV	LLT																																
Consensus	198	EIPEISLP	IIITN	VAKQCY	ERGEK	PKVT	DGDK	VEDPT	FINQ	LQSG	VNWR	IRI	ETQ	KVTK	LDROP	PASG	TALQ	ETIS	F	WLN	LERAL	YRIQ	EKR	RES	PEV	LLT																																
Mm	299	LDILKHGR	RREHAT	VSFD	TG	LKQAL	ETVNDY	NPLMK	DFP	NDLL	SAT	ELDK	I	QALVA	I	FTHL	RKIR	NTKY	P	I	QAL	RLVA	I	SRDL	SSQ	LKVL	GTRK																															
Rn	299	LDILKHGR	RREHAT	VSFD	TG	LKQAL	ETVNDY	NPLMK	DFP	NDLL	SAT	ELDK	I	QALVA	I	FTHL	RKIR	NTKY	P	I	QAL	RLVA	I	SRDL	SSQ	LKVL	GTRK																															
Hs	301	LDILKHGR	RREHAT	VSFD	TG	LKQAL	ETVNDY	NPLMK	DFP	NDLL	SAT	ELDK	I	QALVA	I	FTHL	RKIR	NTKY	P	I	QAL	RLVA	I	SRDL	SSQ	LKVL	GTRK																															
Consensus	298	LDILKHGR	RREHAT	VSFD	TG	LKQAL	ETVNDY	NPLMK	DFP	NDLL	SAT	ELDK	I	QALVA	I	FTHL	RKIR	NTKY	P	I	QAL	RLVA	I	SRDL	SSQ	LKVL	GTRK																															
Mm	399	LMHVAYE	EFKVA	VACF	EV	FQ	TWD	DEY	EKLQ	VLL	RD	I	VKKR	RE	NLKN	WRI	NP	AAHKLQ	ARLD	QMR	KERR	Q	EO	LR	AVI	VR	VR	LR	PO	VT	AV	AAQ	QGE	AP																								
Rn	399	LMHVAYE	EFKVA	VACF	EV	FQ	TWD	DEY	EKLQ	VLL	RD	I	VKKR	RE	NLKN	WRI	NP	AAHKLQ	ARLD	QMR	KERR	Q	EO	LR	AVI	VR	VR	LR	PO	VT	AV	AAQ	QGE	AP																								
Hs	401	LMHVAYE	EFKVA	VACF	EV	FQ	TWD	DEY	EKLQ	VLL	RD	I	VKKR	RE	NLKN	WRI	NP	AAHKLQ	ARLD	QMR	KERR	Q	EO	LR	AVI	VR	VR	LR	PO	VT	AV	AAQ	QGE	AP																								
Consensus	398	LMHVAYE	EFKVA	VACF	EV	FQ	TWD	DEY	EKLQ	VLL	RD	I	VKKR	RE	NLKN	WRI	NP	AAHKLQ	ARLD	QMR	KERR	Q	EO	LR	AVI	VR	VR	LR	PO	VT	AV	AAQ	QGE	AP																								
Mm	499	EPQDMK	VAEVL	FD	DA	DANA	IE	EV	NLAY	EN	VE	VD	GL	VS	SK	GT	EA	EA	AM	KRY	D	RI	DR	VE	TR	I	TA	RL	DR	Q	L	G	T	A	K	N	A	N	E	M	E	R	I	F	S	R	F	N	A	L	F	V	R	P	H	I	R	G
Rn	499	EPQDMK	VAEVL	FD	DA	DANA	IE	EV	NLAY	EN	VE	VD	GL	VS	SK	GT	EA	EA	AM	KRY	D	RI	DR	VE	TR	I	TA	RL	DR	Q	L	G	T	A	K	N	A	N	E	M	E	R	I	F	S	R	F	N	A	L	F	V	R	P	H	I	R	G
Hs	501	EPQDMK	VAEVL	FD	DA	DANA	IE	EV	NLAY	EN	VE	VD	GL	VS	SK	GT	EA	EA	AM	KRY	D	RI	DR	VE	TR	I	TA	RL	DR	Q	L	G	T	A	K	N	A	N	E	M	E	R	I	F	S	R	F	N	A	L	F	V	R	P	H	I	R	G
Consensus	498	EPQDMK	VAEVL	FD	DA	DANA	IE	EV	NLAY	EN	VE	VD	GL	VS	SK	GT	EA	EA	AM	KRY	D	RI	DR	VE	TR	I	TA	RL	DR	Q	L	G	T	A	K	N	A	N	E	M	E	R	I	F	S	R	F	N	A	L	F	V	R	P	H	I	R	G

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(Figure 10 continued)

Mm	599	IREYQTQLIQRVKDDI	ESLHDKFKVQYPOQACKSHVRLDPPVSGSIIIAKQIDRLQATAYKRRVEDVLGKGWENHVEGQKLDGDSFRKLNTOEIFD
Rn	599	IREYQTQLIQRVKDDI	ESLHDKFKVQYPOQACKSHVRLDPPVSGSIIIAKQIDRLQATAYKRRVEDVLGKGWENHVEGQKLDGDSFRKLNTOEIFD
Hs	601	IREYQTQLIQRVKDDI	ESLHDKFKVQYPOQACKSHVRLDPPVSGSIIIAKQIDRLQATAYKRRVEDVLGKGWENHVEGQKLDGDSFRKLNTOEIFD
Consensus	598	IREYQTQLIQRVKDDI	ESLHDKFKVQYPOQACKSHVRLDPPVSGSIIIAKQIDRLQATAYKRRVEDVLGKGWENHVEGQKLDGDSFRKLNTOEIFD
Mm	699	QWARKVQQRNLGVSGR	FTTIESARVRGRTGNLKLKVNELPELITLSKVRNLKWLGRVPLAIVNKAHQANQLYPFAISLIESVRYTERTCEKVEERN
Rn	699	QWARKVQQRNLGVSGR	FTTIESARVRGRTGNLKLKVNELPELITLSKVRNLKWLGRVPLAIVNKAHQANQLYPFAISLIESVRYTERTCEKVEERN
Hs	701	QWARKVQQRNLGVSGR	FTTIESARVRGRTGNLKLKVNELPELITLSKVRNLKWLGRVPLAIVNKAHQANQLYPFAISLIESVRYTERTCEKVEERN
Consensus	698	QWARKVQQRNLGVSGR	FTTIESARVRGRTGNLKLKVNELPELITLSKVRNLKWLGRVPLAIVNKAHQANQLYPFAISLIESVRYTERTCEKVEERN
Mm	799	ISLLVAGLKRKEVQALI	AEQFALWESYKLDPPVQVRLAETVFNFEQKQVDDLLIEEKIDLEVSLETCNDYDHTFTSEILNRVQKAVDDLNHLSYSNLP
Rn	799	ISLLVAGLKRKEVQALI	AEQFALWESYKLDPPVQVRLAETVFNFEQKQVDDLLIEEKIDLEVSLETCNDYDHTFTSEILNRVQKAVDDLNHLSYSNLP
Hs	801	ISLLVAGLKRKEVQALI	AEQFALWESYKLDPPVQVRLAETVFNFEQKQVDDLLIEEKIDLEVSLETCNDYDHTFTSEILNRVQKAVDDLNHLSYSNLP
Consensus	798	ISLLVAGLKRKEVQALI	AEQFALWESYKLDPPVQVRLAETVFNFEQKQVDDLLIEEKIDLEVSLETCNDYDHTFTSEILNRVQKAVDDLNHLSYSNLP
Mm	899	NKLDMEIERILGVRLQAGLR	AWTQVLLGQAEQKAEVDMDTDAPOVSHKGGEPKIKNVVHELRTNOVLYLNPPIIEECRYKLYQEMFAMKVVLSLPRIO
Rn	899	NKLDMEIERILGVRLQAGLR	AWTQVLLGQAEQKAEVDMDTDAPOVSHKGGEPKIKNVVHELRTNOVLYLNPPIIEECRYKLYQEMFAMKVVLSLPRIO
Hs	901	NKLDMEIERILGVRLQAGLR	AWTQVLLGQAEQKAEVDMDTDAPOVSHKGGEPKIKNVVHELRTNOVLYLNPPIIEECRYKLYQEMFAMKVVLSLPRIO
Consensus	898	NKLDMEIERILGVRLQAGLR	AWTQVLLGQAEQKAEVDMDTDAPOVSHKGGEPKIKNVVHELRTNOVLYLNPPIIEECRYKLYQEMFAMKVVLSLPRIO
Mm	999	SQRYQGVVHYELTEEEKFYRNAL	TRMPDGPVVALEESYSAVNGIVTEVEQYKVMVLYQYQCLMDMQAENIYNRLGEDLNKQVALLVQIRKARGTDFDNETKK
Rn	999	SQRYQGVVHYELTEEEKFYRNAL	TRMPDGPVVALEESYSAVNGIVTEVEQYKVMVLYQYQCLMDMQAENIYNRLGEDLNKQVALLVQIRKARGTDFDNETKK
Hs	1001	SQRYQGVVHYELTEEEKFYRNAL	TRMPDGPVVALEESYSAVNGIVTEVEQYKVMVLYQYQCLMDMQAENIYNRLGEDLNKQVALLVQIRKARGTDFDNETKK
Consensus	997	SQRYQGVVHYELTEEEKFYRNAL	TRMPDGPVVALEESYSAVNGIVTEVEQYKVMVLYQYQCLMDMQAENIYNRLGEDLNKQVALLVQIRKARGTDFDNETKK
Mm	1099	EFGPWVIDYGRVQSVNLYK	YSWHKEVLSKFCQMLGNSNTEFHSQISKSQBLEQHSVDASTSDAVTITTVQSLKRIKQFEKQVLEYRNGQRLLKQ
Rn	1099	EFGPWVIDYGRVQSVNLYK	YSWHKEVLSKFCQMLGNSNTEFHSQISKSQBLEQHSVDASTSDAVTITTVQSLKRIKQFEKQVLEYRNGQRLLKQ
Hs	1101	EFGPWVIDYGRVQSVNLYK	YSWHKEVLSKFCQMLGNSNTEFHSQISKSQBLEQHSVDASTSDAVTITTVQSLKRIKQFEKQVLEYRNGQRLLKQ
Consensus	1097	EFGPWVIDYGRVQSVNLYK	YSWHKEVLSKFCQMLGNSNTEFHSQISKSQBLEQHSVDASTSDAVTITTVQSLKRIKQFEKQVLEYRNGQRLLKQ
Mm	1199	RFQPPSWLYLDNTEG	WGAFTDNRKDSATQQQVANLQMKIVQEDRAVESRTDLDLTDEKTRPVTGNLPEEALQALTIYEGFGRLLKDDREKCAKA
Rn	1199	RFQPPSWLYLDNTEG	WGAFTDNRKDSATQQQVANLQMKIVQEDRAVESRTDLDLTDEKTRPVTGNLPEEALQALTIYEGFGRLLKDDREKCAKA
Hs	1201	RFQPPSWLYLDNTEG	WGAFTDNRKDSATQQQVANLQMKIVQEDRAVESRTDLDLTDEKTRPVTGNLPEEALQALTIYEGFGRLLKDDREKCAKA
Consensus	1197	RFQPPSWLYLDNTEG	WGAFTDNRKDSATQQQVANLQMKIVQEDRAVESRTDLDLTDEKTRPVTGNLPEEALQALTIYEGFGRLLKDDREKCAKA
Mm	1299	KEALELDTGTLGSGSEER	VQVVALEELQDLKGWSELKSWWQIDQMKQPPWVSVQPRKRLQRLDGLLQNLKRPAPRLROYASVEFVQRLKGGYKNTNMLV
Rn	1299	KEALELDTGTLGSGSEER	VQVVALEELQDLKGWSELKSWWQIDQMKQPPWVSVQPRKRLQRLDGLLQNLKRPAPRLROYASVEFVQRLKGGYKNTNMLV
Hs	1301	KEALELDTGTLGSGSEER	VQVVALEELQDLKGWSELKSWWQIDQMKQPPWVSVQPRKRLQRLDGLLQNLKRPAPRLROYASVEFVQRLKGGYKNTNMLV
Consensus	1297	KEALELDTGTLGSGSEER	VQVVALEELQDLKGWSELKSWWQIDQMKQPPWVSVQPRKRLQRLDGLLQNLKRPAPRLROYASVEFVQRLKGGYKNTNMLV
Mm	1399	TELKSEALKDRHWKQ	LMKRLHVNWVSELTTLGQIDVDVLDIQKNEAKVQKDVLLVAQCEMALIEELKQIREVNTYELDLNRYQNKCRILIRGWDLLFNKVKKEH
Rn	1399	TELKSEALKDRHWKQ	LMKRLHVNWVSELTTLGQIDVDVLDIQKNEAKVQKDVLLVAQCEMALIEELKQIREVNTYELDLNRYQNKCRILIRGWDLLFNKVKKEH
Hs	1401	TELKSEALKDRHWKQ	LMKRLHVNWVSELTTLGQIDVDVLDIQKNEAKVQKDVLLVAQCEMALIEELKQIREVNTYELDLNRYQNKCRILIRGWDLLFNKVKKEH
Consensus	1397	TELKSEALKDRHWKQ	LMKRLHVNWVSELTTLGQIDVDVLDIQKNEAKVQKDVLLVAQCEMALIEELKQIREVNTYELDLNRYQNKCRILIRGWDLLFNKVKKEH
Mm	1499	INSVSANKLS	SPYKVFEDALSWEKLNRIKALFDVWIDVQRRWVYLEGITFGSDIKHLIIVETQFQSIISTEFALMKKVKSKSLPMDVNLNIQGVQRS
Rn	1499	INSVSANKLS	SPYKVFEDALSWEKLNRIKALFDVWIDVQRRWVYLEGITFGSDIKHLIIVETQFQSIISTEFALMKKVKSKSLPMDVNLNIQGVQRS
Hs	1501	INSVSANKLS	SPYKVFEDALSWEKLNRIKALFDVWIDVQRRWVYLEGITFGSDIKHLIIVETQFQSIISTEFALMKKVKSKSLPMDVNLNIQGVQRS
Consensus	1496	INSVSANKLS	SPYKVFEDALSWEKLNRIKALFDVWIDVQRRWVYLEGITFGSDIKHLIIVETQFQSIISTEFALMKKVKSKSLPMDVNLNIQGVQRS

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(Figure 10 continued)

Mm	1599	LERADLLGKIQAALGEYLERERSPPRYFVGDDELLLEIGNSKRVAKLQKFKKMFAGVSSIIINEQSNVVLGTSRGEDEVMFKTPVSI TEHPKINE
Rn	1599	LERADLLGKIQAALGEYLERERSPPRYFVGDDELLLEIGNSKRVAKLQKFKKMFAGVSSIIINEQSNVVLGTSRGEDEVMFKTPVSI TEHPKINE
Hs	1601	LERADLLGKIQAALGEYLERERSPPRYFVGDDELLLEIGNSKRVAKLQKFKKMFAGVSSIIINEQSNVVLGTSRGEDEVMFKTPVSI TEHPKINE
Consensus	1596	LERADLLGKIQAALGEYLERERSPPRYFVGDDELLLEIGNSKRVAKLQKFKKMFAGVSSIIINEQSNVVLGTSRGEDEVMFKTPVSI TEHPKINE
Mm	1699	HLTLVEKERNVTLAKLLAESVTEVEIFGKATSDPNTYTMTDKVQAQVWLSAQIAMSBNVENALSNVGGGDDVGPLOSIVSNVETLVNVLADSVIMEQ
Rn	1699	HLTLVEKERNVTLAKLLAESVTEVEIFGKATSDPNTYTMTDKVQAQVWLSAQIAMSBNVENALSNVGGGDDVGPLOSIVSNVETLVNVLADSVIMEQ
Hs	1701	HLTLVEKERNVTLAKLLAESVTEVEIFGKATSDPNTYTMTDKVQAQVWLSAQIAMSBNVENALSNVGGGDDVGPLOSIVSNVETLVNVLADSVIMEQ
Consensus	1696	HLTLVEKERNVTLAKLLAESVTEVEIFGKATSDPNTYTMTDKVQAQVWLSAQIAMSBNVENALSNVGGGDDVGPLOSIVSNVETLVNVLADSVIMEQ
Mm	1799	PLRRRKLHLITELVHQDVTRSLIKSIDNAKSEWLSQMRFXFDPKQTDVLIQQLSIQMANAKNNGFYEXLGVQDKLVQVLTQRCYLTMTQALEARL
Rn	1799	PLRRRKLHLITELVHQDVTRSLIKSIDNAKSEWLSQMRFXFDPKQTDVLIQQLSIQMANAKNNGFYEXLGVQDKLVQVLTQRCYLTMTQALEARL
Hs	1801	PLRRRKLHLITELVHQDVTRSLIKSIDNAKSEWLSQMRFXFDPKQTDVLIQQLSIQMANAKNNGFYEXLGVQDKLVQVLTQRCYLTMTQALEARL
Consensus	1796	PLRRRKLHLITELVHQDVTRSLIKSIDNAKSEWLSQMRFXFDPKQTDVLIQQLSIQMANAKNNGFYEXLGVQDKLVQVLTQRCYLTMTQALEARL
Mm	1899	GGSPFGPACTGKTESVKALGHQIGREVLVFNCDTEDFQAMGRIFVGLQVQWAGCGFDFENRLEERMLSAVSQVQVCIQALREHNSPNYDKTSAPITCE
Rn	1899	GGSPFGPACTGKTESVKALGHQIGREVLVFNCDTEDFQAMGRIFVGLQVQWAGCGFDFENRLEERMLSAVSQVQVCIQALREHNSPNYDKTSAPITCE
Hs	1901	GGSPFGPACTGKTESVKALGHQIGREVLVFNCDTEDFQAMGRIFVGLQVQWAGCGFDFENRLEERMLSAVSQVQVCIQALREHNSPNYDKTSAPITCE
Consensus	1896	GGSPFGPACTGKTESVKALGHQIGREVLVFNCDTEDFQAMGRIFVGLQVQWAGCGFDFENRLEERMLSAVSQVQVCIQALREHNSPNYDKTSAPITCE
Mm	1999	LINKQVKVSPDMAIFITWMPGVAGRSNLPDNLKILFRSLAMTKPQRLIAQVWLXQGPRTAEVLANKIVPFFKLQDEQLSSQSHYDFGIRALKSVLVA
Rn	1999	LINKQVKVSPDMAIFITWMPGVAGRSNLPDNLKILFRSLAMTKPQRLIAQVWLXQGPRTAEVLANKIVPFFKLQDEQLSSQSHYDFGIRALKSVLVA
Hs	2001	LINKQVKVSPDMAIFITWMPGVAGRSNLPDNLKILFRSLAMTKPQRLIAQVWLXQGPRTAEVLANKIVPFFKLQDEQLSSQSHYDFGIRALKSVLVA
Consensus	1996	LINKQVKVSPDMAIFITWMPGVAGRSNLPDNLKILFRSLAMTKPQRLIAQVWLXQGPRTAEVLANKIVPFFKLQDEQLSSQSHYDFGIRALKSVLVA
Mm	2099	SNVKKRERLOKTKRKEERGEAVDEGEIAENLPEQELLQSVCEWVPKLVAEDIPLIFSLSDVPFGVQYHRCGEMTALREELKKVQCMYLTVDGDEEVG
Rn	2099	SNVKKRERLOKTKRKEERGEAVDEGEIAENLPEQELLQSVCEWVPKLVAEDIPLIFSLSDVPFGVQYHRCGEMTALREELKKVQCMYLTVDGDEEVG
Hs	2101	SNVKKRERLOKTKRKEERGEAVDEGEIAENLPEQELLQSVCEWVPKLVAEDIPLIFSLSDVPFGVQYHRCGEMTALREELKKVQCMYLTVDGDEEVG
Consensus	2096	SNVKKRERLOKTKRKEERGEAVDEGEIAENLPEQELLQSVCEWVPKLVAEDIPLIFSLSDVPFGVQYHRCGEMTALREELKKVQCMYLTVDGDEEVG
Mm	2199	SNVVEKVLQLYQITQINHGIMMVGPSGSKSAMRVLLKALERLSEGVGAHIIIDPKALSKDHLXCTLDPNTREMTDGLFTHVLKRIIDNVGELQKRW
Rn	2199	SNVVEKVLQLYQITQINHGIMMVGPSGSKSAMRVLLKALERLSEGVGAHIIIDPKALSKDHLXCTLDPNTREMTDGLFTHVLKRIIDNVGELQKRW
Hs	2201	SNVVEKVLQLYQITQINHGIMMVGPSGSKSAMRVLLKALERLSEGVGAHIIIDPKALSKDHLXCTLDPNTREMTDGLFTHVLKRIIDNVGELQKRW
Consensus	2196	SNVVEKVLQLYQITQINHGIMMVGPSGSKSAMRVLLKALERLSEGVGAHIIIDPKALSKDHLXCTLDPNTREMTDGLFTHVLKRIIDNVGELQKRW
Mm	2299	LVFDGVDPEWVENLNSVLDNKKLTLNGERLSLPPNVRIMFEVQDLKYATLATVSRGGMVWFSEDLVSTDMIFNNFLARLSIPLDGEDEAQRKRG
Rn	2299	LVFDGVDPEWVENLNSVLDNKKLTLNGERLSLPPNVRIMFEVQDLKYATLATVSRGGMVWFSEDLVSTDMIFNNFLARLSIPLDGEDEAQRKRG
Hs	2301	LVFDGVDPEWVENLNSVLDNKKLTLNGERLSLPPNVRIMFEVQDLKYATLATVSRGGMVWFSEDLVSTDMIFNNFLARLSIPLDGEDEAQRKRG
Consensus	2296	LVFDGVDPEWVENLNSVLDNKKLTLNGERLSLPPNVRIMFEVQDLKYATLATVSRGGMVWFSEDLVSTDMIFNNFLARLSIPLDGEDEAQRKRG
Mm	2399	KEDEGEAAASPMLOIQORDAATIMQPYFTSNGLVTKALEHAFKLEHIMDLTRLCIGLSFMSHQACRNVAQVNAHPDPFPMQIEQLERYIQRVLVVAIILW
Rn	2399	KEDEGEAAASPMLOIQORDAATIMQPYFTSNGLVTKALEHAFKLEHIMDLTRLCIGLSFMSHQACRNVAQVNAHPDPFPMQIEQLERYIQRVLVVAIILW
Hs	2401	KEDEGEAAASPMLOIQORDAATIMQPYFTSNGLVTKALEHAFKLEHIMDLTRLCIGLSFMSHQACRNVAQVNAHPDPFPMQIEQLERYIQRVLVVAIILW
Consensus	2396	KEDEGEAAASPMLOIQORDAATIMQPYFTSNGLVTKALEHAFKLEHIMDLTRLCIGLSFMSHQACRNVAQVNAHPDPFPMQIEQLERYIQRVLVVAIILW
Mm	2499	SLSGDSRLKMRALGEYIRRTITVPLTPAPNIPIDYEVSTISGESSPQAKVPOIEVETHKVAAPDVVVPTLDTVRHEALLYTWLAEHKRLVLCGPGSGG
Rn	2499	SLSGDSRLKMRALGEYIRRTITVPLTPAPNIPIDYEVSTISGESSPQAKVPOIEVETHKVAAPDVVVPTLDTVRHEALLYTWLAEHKRLVLCGPGSGG
Hs	2501	SLSGDSRLKMRALGEYIRRTITVPLTPAPNIPIDYEVSTISGESSPQAKVPOIEVETHKVAAPDVVVPTLDTVRHEALLYTWLAEHKRLVLCGPGSGG
Consensus	2496	SLSGDSRLKMRALGEYIRRTITVPLTPAPNIPIDYEVSTISGESSPQAKVPOIEVETHKVAAPDVVVPTLDTVRHEALLYTWLAEHKRLVLCGPGSGG

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(Figure 10 continued)

Mm	2599	KTMTLFSALRALPDMEVVGGLNFSSATTPPELLIKTDFHYCEYRRTPNGVVLAVQGLKWLVLFCDEINLPDMDKYGTQVVISFIQWVEHGGFVPTSDQW
Rn	2599	KTMTLFSALRALPDMEVVGGLNFSSATTPPELLIKTDFHYCEYRRTPNGVVLAVQGLKWLVLFCDEINLPDMDKYGTQVVISFIQWVEHGGFVPTSDQW
Hs	2601	KTMTLFSALRALPDMEVVGGLNFSSATTPPELLIKTDFHYCEYRRTPNGVVLAVQGLKWLVLFCDEINLPDMDKYGTQVVISFIQWVEHGGFVPTSDQW
Consensus	2595	KTMTLFSALRALPDMEVVGGLNFSSATTPPELLIKTDFHYCEYRRTPNGVVLAVQGLKWLVLFCDEINLPDMDKYGTQVVISFIQWVEHGGFVPTSDQW
Mm	2699	VKLRIQEVGACNPPTDGRPLSHRFLRHVPVYVDYDGPASLTQIYGTNRAMLRLIPLSRTVAEPLTAAMVEFYTWSQERFTQDTQPHVITYSPREMT
Rn	2699	VKLRIQEVGACNPPTDGRPLSHRFLRHVPVYVDYDGPASLTQIYGTNRAMLRLIPLSRTVAEPLTAAMVEFYTWSQERFTQDTQPHVITYSPREMT
Hs	2699	VKLRIQEVGACNPPTDGRPLSHRFLRHVPVYVDYDGPASLTQIYGTNRAMLRLIPLSRTVAEPLTAAMVEFYTWSQERFTQDTQPHVITYSPREMT
Consensus	2701	VKLRIQEVGACNPPTDGRPLSHRFLRHVPVYVDYDGPASLTQIYGTNRAMLRLIPLSRTVAEPLTAAMVEFYTWSQERFTQDTQPHVITYSPREMT
Mm	2799	RWVGIFFEALRPLETLPVEGLIRIWAHEALRFDRLVEDEERWTQDENIDMVALKHPNIDKEKAMSRPILYSNWLSDXYIPVDOEELRDYVKARLKV
Rn	2799	RWVGIFFEALRPLETLPVEGLIRIWAHEALRFDRLVEDEERWTQDENIDMVALKHPNIDKEKAMSRPILYSNWLSDXYIPVDOEELRDYVKARLKV
Hs	2801	RWVGIFFEALRPLETLPVEGLIRIWAHEALRFDRLVEDEERWTQDENIDMVALKHPNIDKEKAMSRPILYSNWLSDXYIPVDOEELRDYVKARLKV
Consensus	2795	RWVGIFFEALRPLETLPVEGLIRIWAHEALRFDRLVEDEERWTQDENIDMVALKHPNIDKEKAMSRPILYSNWLSDXYIPVDOEELRDYVKARLKV
Mm	2899	YEELDVPLVLFNEVLQHVLRIDRIFRQPOGHLLIGVSGAGKTTLSRFVAMMGLSVYQIKVHKYTGEDFEDDLRTVLRSSGCKNEKIAFIMDES
Rn	2899	YEELDVPLVLFNEVLQHVLRIDRIFRQPOGHLLIGVSGAGKTTLSRFVAMMGLSVYQIKVHKYTGEDFEDDLRTVLRSSGCKNEKIAFIMDES
Hs	2901	YEELDVPLVLFNEVLQHVLRIDRIFRQPOGHLLIGVSGAGKTTLSRFVAMMGLSVYQIKVHKYTGEDFEDDLRTVLRSSGCKNEKIAFIMDES
Consensus	2895	YEELDVPLVLFNEVLQHVLRIDRIFRQPOGHLLIGVSGAGKTTLSRFVAMMGLSVYQIKVHKYTGEDFEDDLRTVLRSSGCKNEKIAFIMDES
Mm	2999	DSGFLENNMTLLANGVEVPGIFEGDEVATLQCKEAGKGLMLDSHEELKWTQSOVIRNLHVVTWNPSSSEGKDKRAATSPALFNRCLVNWFGDMSTE
Rn	2999	DSGFLENNMTLLANGVEVPGIFEGDEVATLQCKEAGKGLMLDSHEELKWTQSOVIRNLHVVTWNPSSSEGKDKRAATSPALFNRCLVNWFGDMSTE
Hs	3001	DSGFLENNMTLLANGVEVPGIFEGDEVATLQCKEAGKGLMLDSHEELKWTQSOVIRNLHVVTWNPSSSEGKDKRAATSPALFNRCLVNWFGDMSTE
Consensus	2995	DSGFLENNMTLLANGVEVPGIFEGDEVATLQCKEAGKGLMLDSHEELKWTQSOVIRNLHVVTWNPSSSEGKDKRAATSPALFNRCLVNWFGDMSTE
Mm	3099	ALYQVGEFTSKMDLEKPNYIVPDYMPVYVDKLPQPPHREAIWVSCVFVHQTLOHANAALAKRGGRMTATPRHYLDFINHYANLFHEKSELEEQQMH
Rn	3099	ALYQVGEFTSKMDLEKPNYIVPDYMPVYVDKLPQPPHREAIWVSCVFVHQTLOHANAALAKRGGRMTATPRHYLDFINHYANLFHEKSELEEQQMH
Hs	3101	ALYQVGEFTSKMDLEKPNYIVPDYMPVYVDKLPQPPHREAIWVSCVFVHQTLOHANAALAKRGGRMTATPRHYLDFINHYANLFHEKSELEEQQMH
Consensus	3095	ALYQVGEFTSKMDLEKPNYIVPDYMPVYVDKLPQPPHREAIWVSCVFVHQTLOHANAALAKRGGRMTATPRHYLDFINHYANLFHEKSELEEQQMH
Mm	3199	LAVGLRRIKETVDQVEELRDLRIKSOELEVNRNAAANDKLKMKVQDQOEAKKKVMSQETQEQHLKQEVIAQKQMSWKEDLDKVEPAVIEAQNAAVKS
Rn	3199	LAVGLRRIKETVDQVEELRDLRIKSOELEVNRNAAANDKLKMKVQDQOEAKKKVMSQETQEQHLKQEVIAQKQMSWKEDLDKVEPAVIEAQNAAVKS
Hs	3201	LAVGLRRIKETVDQVEELRDLRIKSOELEVNRNAAANDKLKMKVQDQOEAKKKVMSQETQEQHLKQEVIAQKQMSWKEDLDKVEPAVIEAQNAAVKS
Consensus	3195	LAVGLRRIKETVDQVEELRDLRIKSOELEVNRNAAANDKLKMKVQDQOEAKKKVMSQETQEQHLKQEVIAQKQMSWKEDLDKVEPAVIEAQNAAVKS
Mm	3299	KQHLVRSNANPPAAVKLALESICLLLGESTTDMKQIRSIIMRENFIPTIVNFSABEISDAIREKKKNYNSPNSYNYEIVNRASLACGGPMVKWALAQ
Rn	3299	KQHLVRSNANPPAAVKLALESICLLLGESTTDMKQIRSIIMRENFIPTIVNFSABEISDAIREKKKNYNSPNSYNYEIVNRASLACGGPMVKWALAQ
Hs	3301	KQHLVRSNANPPAAVKLALESICLLLGESTTDMKQIRSIIMRENFIPTIVNFSABEISDAIREKKKNYNSPNSYNYEIVNRASLACGGPMVKWALAQ
Consensus	3295	KQHLVRSNANPPAAVKLALESICLLLGESTTDMKQIRSIIMRENFIPTIVNFSABEISDAIREKKKNYNSPNSYNYEIVNRASLACGGPMVKWALAQ
Mm	3399	NYADMVKRVEPLRNELOKLEDDAKDQKQKANEVQMIROLEASIAKYKEEYAVLISEAQAIKADLAVERKVNRSSTALLKSLSAERERWKTSETFRNQ
Rn	3399	NYADMVKRVEPLRNELOKLEDDAKDQKQKANEVQMIROLEASIAKYKEEYAVLISEAQAIKADLAVERKVNRSSTALLKSLSAERERWKTSETFRNQ
Hs	3401	NYADMVKRVEPLRNELOKLEDDAKDQKQKANEVQMIROLEASIAKYKEEYAVLISEAQAIKADLAVERKVNRSSTALLKSLSAERERWKTSETFRNQ
Consensus	3395	NYADMVKRVEPLRNELOKLEDDAKDQKQKANEVQMIROLEASIAKYKEEYAVLISEAQAIKADLAVERKVNRSSTALLKSLSAERERWKTSETFRNQ
Mm	3499	STIAGDCLLSAAFIAYAGYEDQDMQNLFETWSSHLLQQANIQERTDIARTXYLSNADERLRWQASSIPADDLCTENAIMLKRNRYPLIIDPSCQATEFI
Rn	3499	STIAGDCLLSAAFIAYAGYEDQDMQNLFETWSSHLLQQANIQERTDIARTXYLSNADERLRWQASSIPADDLCTENAIMLKRNRYPLIIDPSCQATEFI
Hs	3501	STIAGDCLLSAAFIAYAGYEDQDMQNLFETWSSHLLQQANIQERTDIARTXYLSNADERLRWQASSIPADDLCTENAIMLKRNRYPLIIDPSCQATEFI
Consensus	3495	STIAGDCLLSAAFIAYAGYEDQDMQNLFETWSSHLLQQANIQERTDIARTXYLSNADERLRWQASSIPADDLCTENAIMLKRNRYPLIIDPSCQATEFI

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(Figure 10 continued)

Mm	3599	YNEYKDKRI	TRTSFLDDA	FRKNLESAL	RFCGNPLIVQ	DESYPV	INPVLN	REVRTGR	VLTIGD	QDIDLS	PSFV	FLST	RDPT	VEPP	PDLC	SRVTEV
Rn	3599	YNEYKDKRI	TRTSFLDDA	FRKNLESAL	RFCGNPLIVQ	DESYPV	INPVLN	REVRTGR	VLTIGD	QDIDLS	PSFV	FLST	RDPT	VEPP	PDLC	SRVTEV
Hs	3601	YNEYKDKRI	TRTSFLDDA	FRKNLESAL	RFCGNPLIVQ	DESYPV	INPVLN	REVRTGR	VLTIGD	QDIDLS	PSFV	FLST	RDPT	VEPP	PDLC	SRVTEV
Consensus	3595	YNEYKDKRI	TRTSFLDDA	FRKNLESAL	RFCGNPLIVQ	DESYPV	INPVLN	REVRTGR	VLTIGD	QDIDLS	PSFV	FLST	RDPT	VEPP	PDLC	SRVTEV
Mm	3699	FTWTRSS	LOSQC	NEVLKAE	RPVDKRS	DLKLALQ	SEFO	LRQLK	ESLLQ	ALNEV	GRIL	DDT	IT	IT	IT	IT
Rn	3699	FTWTRSS	LOSQC	NEVLKAE	RPVDKRS	DLKLALQ	SEFO	LRQLK	ESLLQ	ALNEV	GRIL	DDT	IT	IT	IT	IT
Hs	3701	FTWTRSS	LOSQC	NEVLKAE	RPVDKRS	DLKLALQ	SEFO	LRQLK	ESLLQ	ALNEV	GRIL	DDT	IT	IT	IT	IT
Consensus	3695	FTWTRSS	LOSQC	NEVLKAE	RPVDKRS	DLKLALQ	SEFO	LRQLK	ESLLQ	ALNEV	GRIL	DDT	IT	IT	IT	IT
Mm	3799	YLPSTAC	SSIYFT	MSLKV	HFY	YSLQ	FFDI	YHN	VLYEN	PNL	KGAT	DHT	QRL	SVI	IT	IT
Rn	3799	YLPSTAC	SSIYFT	MSLKV	HFY	YSLQ	FFDI	YHN	VLYEN	PNL	KGAT	DHT	QRL	SVI	IT	IT
Hs	3801	YLPSTAC	SSIYFT	MSLKV	HFY	YSLQ	FFDI	YHN	VLYEN	PNL	KGAT	DHT	QRL	SVI	IT	IT
Consensus	3795	YLPSTAC	SSIYFT	MSLKV	HFY	YSLQ	FFDI	YHN	VLYEN	PNL	KGAT	DHT	QRL	SVI	IT	IT
Mm	3899	YDAEFQ	HF	LRG	KEIV	LSAG	STPK	IO	GLT	VEQ	AEAV	RLS	CLP	AK	DI	IA
Rn	3899	YDAEFQ	HF	LRG	KEIV	LSAG	STPK	IO	GLT	VEQ	AEAV	RLS	CLP	AK	DI	IA
Hs	3901	YDAEFQ	HF	LRG	KEIV	LSAG	STPK	IO	GLT	VEQ	AEAV	RLS	CLP	AK	DI	IA
Consensus	3893	YDAEFQ	HF	LRG	KEIV	LSAG	STPK	IO	GLT	VEQ	AEAV	RLS	CLP	AK	DI	IA
Mm	3999	YLANAH	MFVST	NL	GES	FMS	INEQ	PLDI	TH	VG	TEV	KPNT	VL	MC	SV	PG
Rn	3999	YLANAH	MFVST	NL	GES	FMS	INEQ	PLDI	TH	VG	TEV	KPNT	VL	MC	SV	PG
Hs	4001	YLANAH	MFVST	NL	GES	FMS	INEQ	PLDI	TH	VG	TEV	KPNT	VL	MC	SV	PG
Consensus	3991	YLANAH	MFVST	NL	GES	FMS	INEQ	PLDI	TH	VG	TEV	KPNT	VL	MC	SV	PG
Mm	4099	LAPG	WM	QLEK	KL	HS	LQ	PH	AC	FE	LT	ME	IN	KV	PV	LL
Rn	4099	LAPG	WM	QLEK	KL	HS	LQ	PH	AC	FE	LT	ME	IN	KV	PV	LL
Hs	4101	LAPG	WM	QLEK	KL	HS	LQ	PH	AC	FE	LT	ME	IN	KV	PV	LL
Consensus	4091	LAPG	WM	QLEK	KL	HS	LQ	PH	AC	FE	LT	ME	IN	KV	PV	LL
Mm	4199	YSKKY	EFG	ES	DL	RS	AC	DT	VD	TW	LD	DD	TAK	GR	QNI	SP
Rn	4199	YSKKY	EFG	ES	DL	RS	AC	DT	VD	TW	LD	DD	TAK	GR	QNI	SP
Hs	4201	YSKKY	EFG	ES	DL	RS	AC	DT	VD	TW	LD	DD	TAK	GR	QNI	SP
Consensus	4190	YSKKY	EFG	ES	DL	RS	AC	DT	VD	TW	LD	DD	TAK	GR	QNI	SP
Mm	4299	RREE	FQ	W	VEL	L	P	D	A	Q	T	P	S	R	L	G
Rn	4299	RREE	FQ	W	VEL	L	P	D	A	Q	T	P	S	R	L	G
Hs	4301	RREE	FQ	W	VEL	L	P	D	A	Q	T	P	S	R	L	G
Consensus	4290	RREE	FQ	W	VEL	L	P	D	A	Q	T	P	S	R	L	G
Mm	4399	YVEN	I	K	D	P	L	F	R	E	F	E	R	V	K	G
Rn	4399	YVEN	I	K	D	P	L	F	R	E	F	E	R	V	K	G
Hs	4401	YVEN	I	K	D	P	L	F	R	E	F	E	R	V	K	G
Consensus	4390	YVEN	I	K	D	P	L	F	R	E	F	E	R	V	K	G

(Figure 10 continued)

Mm	4499	AKELKNIHVCLGGLFVPEAYITATROYVAQANSWSLEELCLEVNVVTASQSATLDACSGVGTGKLOGATCSNNKLSLSNAISTVLPLTQLRWVKQTSAEK
Rn	4499	AKELKNIHVCLGGLFVPEAYITATROYVAQANSWSLEELCLEVNVVTASQSATLDACSGVGTGKLOGATCSNNKLSLSNAISTVLPLTQLRWVKQTSAEK
Hs	4501	AKELKNIHVCLGGLFVPEAYITATROYVAQANSWSLEELCLEVNVVTASQSATLDACSGVGTGKLOGATCSNNKLSLSNAISTVLPLTQLRWVKQTSAEK
Consensus	4490	AKELKNIHVCLGGLFVPEAYITATROYVAQANSWSLEELCLEVNVVTASQSATLDACSGVGTGKLOGATCSNNKLSLSNAISTVLPLTQLRWVKQTSAEK
Mm	4599	KASVVTLPVYLNFTRADLIFTVDFFEATKEDPRSFYERGVAVLCTE
Rn	4599	KASVVTLPVYLNFTRADLIFTVDFFEATKEDPRSFYERGVAVLCTE
Hs	4601	KASVVTLPVYLNFTRADLIFTVDFFEATKEDPRSFYERGVAVLCTE
Consensus	4590	KASVVTLPVYLNFTRADLIFTVDFFEATKEDPRSFYERGVAVLCTE

Percentage of identical amino acid residues: 95%

Percentage of identical and similar amino acid residues: 96%

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Figure 11. Amino Acid Alignment of Mouse, and Human Dynein Intermediate Chain 1 Proteins –Highly Conserved Amino Acid Residues.

Software used:

- MultAlin via <http://prodes.toulouse.inra.fr/multalin/multalin.html> [Corpet. F. (1988), Multiple sequence alignment with hierarchical clustering, Nucl. Acids Res., 16 (22), 10881-10890]
- BOXSHADE 3.21 via http://www.ch.embnet.org/software/BOX_form.html

NP_034193.1 (mouse)	1	MSDKSDLKAELEKRRKQRLAQIREKKRKEERKKKEADMQQKKEPVQDDSDLDKRKRETE
NP_004402.1 (human)	1	MSDKSDLKAELEKRRKQRLAQIREKKRKEERKKKEADMQQKKEPVQDDSDLDKRKRETE
Consensus	1	MSDKSDLKAELEKRRKQRLAQIREKKRKEERKKKEADMQQKKEPVQDDSDLDKRKRETE
NP_034193.1 (mouse)	61	ALLQSIGISPEPLV.....PTPMSFSSKSVSTPSHAGSQDSGDLGPI
NP_004402.1 (human)	61	ALLQSIGISPEPLVQPLHFLTWDTCYFHYLVPTPMSFSSKSVSTPSHAGSQDSGDLGPI
Consensus	61	ALLQSIGISPEPLV.....PTPMSFSSKSVSTPSHAGSQDSGDLGPI
NP_034193.1 (mouse)	104	TRTLQWDTPSVLQLQSDSELGRRHLKLGVSQVTVQDFLPREVVSYSKETQTPLATHQSE
NP_004402.1 (human)	121	TRTLQWDTPSVLQLQSDSELGRRHLKLGVSQVTVQDFLPREVVSYSKETQTPLATHQSE
Consensus	103	TRTLQWDTPSVLQLQSDSELGRRHLKLGVSQVTVQDFLPREVVSYSKETQTPLATHQSE
NP_034193.1 (mouse)	164	EDEEDEEMVEPKHGHQDSELENCKKKQETKEAPPRELTEEEKQQILHSEEFLLIFFDRTIRV
NP_004402.1 (human)	181	EDEEDEEMVESKAGQDSELENCKKKQETKEAPPRELTEEEKQQILHSEEFLLIFFDRTIRV
Consensus	163	EDEEDEEMVEPKHGHQDSELENCKKKQETKEAPPRELTEEEKQQILHSEEFLLIFFDRTIRV
NP_034193.1 (mouse)	224	IERALAEDSDIFFDYSGRELEEKDGDVQAGANLSFNRQFYDEHWSKHRVVTCDMSLQYP
NP_004402.1 (human)	241	IERALAEDSDIFFDYSGRELEEKDGDVQAGANLSFNRQFYDEHWSKHRVVTCDMSLQYP
Consensus	221	IERALAEDSDIFFDYSGRELEEKDGDVQAGANLSFNRQFYDEHWSKHRVVTCDMSLQYP
NP_034193.1 (mouse)	284	ELMVASYNNEDAPHEPDGVALVWNMKFKKTTPYVVFHCQSSVMSVCFARFHPNLVVGGT
NP_004402.1 (human)	301	ELMVASYNNEDAPHEPDGVALVWNMKFKKTTPYVVFHCQSSVMSVCFARFHPNLVVGGT
Consensus	281	ELMVASYNNEDAPHEPDGVALVWNMKFKKTTPYVVFHCQSSVMSVCFARFHPNLVVGGT
NP_034193.1 (mouse)	344	YSGQIVLWDRSHRRTPVQRTPLSAAATHPVYCVHVVGTHHARNLITVSTDGKMCWSL
NP_004402.1 (human)	361	YSGQIVLWDRSHRRTPVQRTPLSAAATHPVYCVHVVGTHHARNLITVSTDGKMCWSL
Consensus	341	YSGQIVLWDRSHRRTPVQRTPLSAAATHPVYCVHVVGTHHARNLITVSTDGKMCWSL
NP_034193.1 (mouse)	404	DMLSTPQESMELVYNKSKPVAVTGMAFPTGDVNNFVVGSEEGTVYACRHGSKAGIGEVF
NP_004402.1 (human)	421	DMLSTPQESMELVYNKSKPVAVTGMAFPTGDVNNFVVGSEEGTVYACRHGSKAGIGEVF
Consensus	401	DMLSTPQESMELVYNKSKPVAVTGMAFPTGDVNNFVVGSEEGTVYACRHGSKAGIGEVF
NP_034193.1 (mouse)	464	EGHQGPVTGINCHMAVGPIDFSHLFTSSFDWTVKLWTTKHNKPLYSFEDNADYVYDVMM
NP_004402.1 (human)	481	EGHQGPVTGINCHMAVGPIDFSHLFTSSFDWTVKLWTTKHNKPLYSFEDNADYVYDVMM
Consensus	461	EGHQGPVTGINCHMAVGPIDFSHLFTSSFDWTVKLWTTKHNKPLYSFEDNADYVYDVMM
NP_034193.1 (mouse)	524	SPVHPALFACVDGMGRDLWNLNNDTEVPTASVAIEGASALNRVRWAQAGKEVAVGDSEG
NP_004402.1 (human)	541	SPVHPALFACVDGMGRDLWNLNNDTEVPTASVAIEGASALNRVRWAQAGKEVAVGDSEG
Consensus	521	SPVHPALFACVDGMGRDLWNLNNDTEVPTASVAIEGASALNRVRWAQAGKEVAVGDSEG
NP_034193.1 (mouse)	584	RIWYIDVGELAVPHNDEWTRFARTLVEIRANRADSEEGAVELAA
NP_004402.1 (human)	601	RIWYIDVGELAVPHNDEWTRFARTLVEIRANRADSEEGAVELAA
Consensus	581	RIWYIDVGELAVPHNDEWTRFARTLVEIRANRADSEEGAVELAA

Amino acid identity: 88%

Amino acid similarity: 89%

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Figure 12. Amino Acid Alignment of Mouse, Rattus Norvegicus, and Human Dynein Intermediate Chain1 Proteins –Highly Conserved Amino Acid Residues.

Software used:

MultAlin via <http://prodes.toulouse.inra.fr/multalin/multalin.html> [Corpet. F. (1988), Multiple sequence alignment with hierarchical clustering, Nucl. Acids Res., 16 (22), 10881-10890]

BOXSHADE 3.21 via http://www.ch.embnet.org/software/BOX_form.html

		1M
NP_034193.1(mouse)	1	MSDKSDLKAELEKRRKQRLAQIREKKRKEERKKKEADMQQKEFPVQDDSLDRKRRETE
NP_004402.1(human)	1	MSDKSDLKAELEKRRKQRLAQIREKKRKEERKKKEADMQQKEFPVQDDSLDRKRRETE
NP_062107.1(rat)	1	MSDKSDLKAELEKRRKQRLAQIREKKRKEERKKKEADMQQKEFPVQDDSLDRKRRETE
Consensus	1	MSDKSDLKAELEKRRKQRLAQIREKKRKEERKKKEADMQQKEFPVQDDSLDRKRRETE
NP_034193.1(mouse)	61	ALLQSIGISPEPPLV.....PTPMSPSSKSVSTFSLAGSQDSGDLGPL
NP_004402.1(human)	61	ALLQSIGISPEPPLVQPLHFLTWDTCYFHYLVPTPMSPSSKSVSTFSEAGSQDSGDLGPL
NP_062107.1(rat)	61	ALLQSIGISPEPPLVQPLHFLTWDTCYFHYLVPTPMSPSSKSVSTFSEAGSQD...DLGPL
Consensus	61	ALLQSIGISPEPPLVQPLHFLTWDTCYFHYLVPTPMSPSSKSVSTFSLAGSQDSGDLGPL
		140E 157F 164B 174A
NP_034193.1(mouse)	104	TRTLQWDTPSVLQLQSDSELGRRRLHKLGVSKVTQVDFLPREVVSYSKETQTPLATHQSE
NP_004402.1(human)	121	TRTLQWDTPSVLQLQSDSELGRRRLHKLGVSKVTQVDFLPREVVSYSKETQTPLATHQSE
NP_062107.1(rat)	119	TRTLQWDTPSVLQLQSDSELGRRRLHKLGVSKVTQVDFLPREVVSYSKETQTPLATHQSE
Consensus	120	TRTLQWDTPSVLQLQSDSELGRRRLHKLGVSKVTQVDFLPREVVSYSKETQTPLATHQSE
NP_034193.1(mouse)	164	EDEEDEEMVEPFGHDSLELNCNKKQETKEAPPRELTEEEKQQLHSEEFLLIFFDRTIRV
NP_004402.1(human)	181	EDEEDEEMVEPFGHDSLELNCNKKQETKEAPPRELTEEEKQQLHSEEFLLIFFDRTIRV
NP_062107.1(rat)	179	EDEEDEEMVEPFGHDSLELNCNKKQETKEAPPRELTEEEKQQLHSEEFLLIFFDRTIRV
Consensus	180	EDEEDEEMVEPFGHDSLELNCNKKQETKEAPPRELTEEEKQQLHSEEFLLIFFDRTIRV
		260L
NP_034193.1(mouse)	224	IERALAEDSDIFFDYSGRELEEKDGDVQAGANLSFNRFYDEHWSKHRVVTCDWLSLQYP
NP_004402.1(human)	241	IERALAEDSDIFFDYSGRELEEKDGDVQAGANLSFNRFYDEHWSKHRVVTCDWLSLQYP
NP_062107.1(rat)	239	IERALAEDSDIFFDYSGRELEEKDGDVQAGANLSFNRFYDEHWSKHRVVTCDWLSLQYP
Consensus	238	IERALAEDSDIFFDYSGRELEEKDGDVQAGANLSFNRFYDEHWSKHRVVTCDWLSLQYP
		331T
NP_034193.1(mouse)	284	ELMVASYSNNEDAPHEPDGVALVWNMKFKKTTPEYVFHCQSSVMSVCFARFHPNLVVGGT
NP_004402.1(human)	301	ELMVASYSNNEDAPHEPDGVALVWNMKFKKTTPEYVFHCQSSVMSVCFARFHPNLVVGGT
NP_062107.1(rat)	299	ELMVASYSNNEDAPHEPDGVALVWNMKFKKTTPEYVFHCQSSVMSVCFARFHPNLVVGGT
Consensus	298	ELMVASYSNNEDAPHEPDGVALVWNMKFKKTTPEYVFHCQSSVMSVCFARFHPNLVVGGT
NP_034193.1(mouse)	344	YSGQIVLWDNRSHRRTPVQRTPLSAAATHPVYCVNVVGTQNAHNLITVSTDGKNCWSL
NP_004402.1(human)	361	YSGQIVLWDNRSHRRTPVQRTPLSAAATHPVYCVNVVGTQNAHNLITVSTDGKNCWSL
NP_062107.1(rat)	359	YSGQIVLWDNRSHRRTPVQRTPLSAAATHPVYCVNVVGTQNAHNLITVSTDGKNCWSL
Consensus	358	YSGQIVLWDNRSHRRTPVQRTPLSAAATHPVYCVNVVGTQNAHNLITVSTDGKNCWSL
NP_034193.1(mouse)	404	DMLSTPQESMELVYNKSEFPVAVTGMAFPTGDVNNFVVGSEEGTVYTACRHGSKAGIGEVF
NP_004402.1(human)	421	DMLSTPQESMELVYNKSEFPVAVTGMAFPTGDVNNFVVGSEEGTVYTACRHGSKAGIGEVF
NP_062107.1(rat)	419	DMLSTPQESMELVYNKSEFPVAVTGMAFPTGDVNNFVVGSEEGTVYTACRHGSKAGIGEVF
Consensus	418	DMLSTPQESMELVYNKSEFPVAVTGMAFPTGDVNNFVVGSEEGTVYTACRHGSKAGIGEVF
NP_034193.1(mouse)	464	EGHQGPVTGINCHMAVGPIDFSHLFTVSSFDWTVLWTTKHNKPLYSFEDNADYVYDVMW
NP_004402.1(human)	481	EGHQGPVTGINCHMAVGPIDFSHLFTVSSFDWTVLWTTKHNKPLYSFEDNADYVYDVMW
NP_062107.1(rat)	479	EGHQGPVTGINCHMAVGPIDFSHLFTVSSFDWTVLWTTKHNKPLYSFEDNADYVYDVMW
Consensus	478	EGHQGPVTGINCHMAVGPIDFSHLFTVSSFDWTVLWTTKHNKPLYSFEDNADYVYDVMW

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(figure 12 continued)

NP_034193.1(mouse)	524	SPVHPALFACVDGMGRDLWNLSNDEVTASVAIEGASALNRVRWAQGGKEVAVGDSEG
NP_004402.1(human)	541	SPVHPALFACVDGMGRDLWNLSNDEVTASVAIEGASALNRVRWAQGGKEVAVGDSEG
NP_062107.1(rat)	539	SPVHPALFACVDGMGRDLWNLSNDEVTASVAIEGASALNRVRWAQGGKEVAVGDSEG
Consensus	538	SPVHPALFACVDGMGRDLWNLSNDEVTASVAIEGASALNRVRWAQGGKEVAVGDSEG
NP_034193.1(mouse)	584	RIWIYDVGELAVPHNDEWTRFARTLVEIRANRADSEEEGAVELAA
NP_004402.1(human)	601	RIWIYDVGELAVPHNDEWTRFARTLVEIRANRADSEEEGAVELAA
NP_062107.1(rat)	599	RIWIYDVGELAVPHNDEWTRFARTLVEIRANRADSEEEGAVELAA
Consensus	598	RIWIYDVGELAVPHNDEWTRFARTLVEIRANRADSEEEGAVELAA

Amino acid identity: 87%
Amino acid similarity: 88%

The following binding domains are indicated by their N-terminal and C-terminal amino acids (positions correspond to the human amino acid sequence):

p150d (DCTN1 (p150) binding domain)	1M – 140E
Tctex1d (Tctex1 binding domain)	157F-174A
10kDad (10kDa light chain binding domain)	164S-174A
2Bd (2B light chain binding domain)	260L-331T

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Figure 13. Amino Acid Alignment of Mouse and Human Dynein Intermediate Chain 2 Proteins –Highly Conserved Amino Acid Residues.

Software used:

- MultAlin via <http://prodes.toulouse.inra.fr/multalin/multalin.html> [Corpet. F. (1988), Multiple sequence alignment with hierarchical clustering, Nucl. Acids Res., 16 (22), 10881-10890]
- BOXSHADE 3.21 via http://www.ch.embnet.org/software/BOX_form.html

NP_034194.1 (mouse)	1	MSDKS	1	MSDKS	1	MSDKS	1	MSDKS
NP_001369.1 (human)	1	MSDKS	1	MSDKS	1	MSDKS	1	MSDKS
Consensus	1	MSDKS	1	MSDKS	1	MSDKS	1	MSDKS
NP_034194.1 (mouse)	61	EALQSMGLT	61	EALQSMGLT	61	EALQSMGLT	61	EALQSMGLT
NP_001369.1 (human)	61	EALQSMGLT	61	EALQSMGLT	61	EALQSMGLT	61	EALQSMGLT
Consensus	60	EALQSMGLT	60	EALQSMGLT	60	EALQSMGLT	60	EALQSMGLT
NP_034194.1 (mouse)	107	107	107	107
NP_001369.1 (human)	121	SVLQLHSDSDLC	121	SVLQLHSDSDLC	121	SVLQLHSDSDLC	121	SVLQLHSDSDLC
Consensus	105	105	105	105
NP_034194.1 (mouse)	155	PKPPPEPEE	155	PKPPPEPEE	155	PKPPPEPEE	155	PKPPPEPEE
NP_001369.1 (human)	181	PKPPPEPEE	181	PKPPPEPEE	181	PKPPPEPEE	181	PKPPPEPEE
Consensus	152	PKPPPEPEE	152	PKPPPEPEE	152	PKPPPEPEE	152	PKPPPEPEE
NP_034194.1 (mouse)	215	INIFFDYSGRDLEDKEGEIQAGAKLSLNRQFFDERWSKHRVVSCLDWSSQYPELLVASYN	215	INIFFDYSGRDLEDKEGEIQAGAKLSLNRQFFDERWSKHRVVSCLDWSSQYPELLVASYN	215	INIFFDYSGRDLEDKEGEIQAGAKLSLNRQFFDERWSKHRVVSCLDWSSQYPELLVASYN	215	INIFFDYSGRDLEDKEGEIQAGAKLSLNRQFFDERWSKHRVVSCLDWSSQYPELLVASYN
NP_001369.1 (human)	241	INIFFDYSGRDLEDKEGEIQAGAKLSLNRQFFDERWSKHRVVSCLDWSSQYPELLVASYN	241	INIFFDYSGRDLEDKEGEIQAGAKLSLNRQFFDERWSKHRVVSCLDWSSQYPELLVASYN	241	INIFFDYSGRDLEDKEGEIQAGAKLSLNRQFFDERWSKHRVVSCLDWSSQYPELLVASYN	241	INIFFDYSGRDLEDKEGEIQAGAKLSLNRQFFDERWSKHRVVSCLDWSSQYPELLVASYN
Consensus	211	INIFFDYSGRDLEDKEGEIQAGAKLSLNRQFFDERWSKHRVVSCLDWSSQYPELLVASYN	211	INIFFDYSGRDLEDKEGEIQAGAKLSLNRQFFDERWSKHRVVSCLDWSSQYPELLVASYN	211	INIFFDYSGRDLEDKEGEIQAGAKLSLNRQFFDERWSKHRVVSCLDWSSQYPELLVASYN	211	INIFFDYSGRDLEDKEGEIQAGAKLSLNRQFFDERWSKHRVVSCLDWSSQYPELLVASYN
NP_034194.1 (mouse)	275	NNEEAPHEPDGVALVNMKYKKTTPPEYVHCQSAVMSATFAKFHFNLVVGGTYSQIVLW	275	NNEEAPHEPDGVALVNMKYKKTTPPEYVHCQSAVMSATFAKFHFNLVVGGTYSQIVLW	275	NNEEAPHEPDGVALVNMKYKKTTPPEYVHCQSAVMSATFAKFHFNLVVGGTYSQIVLW	275	NNEEAPHEPDGVALVNMKYKKTTPPEYVHCQSAVMSATFAKFHFNLVVGGTYSQIVLW
NP_001369.1 (human)	301	NNEEAPHEPDGVALVNMKYKKTTPPEYVHCQSAVMSATFAKFHFNLVVGGTYSQIVLW	301	NNEEAPHEPDGVALVNMKYKKTTPPEYVHCQSAVMSATFAKFHFNLVVGGTYSQIVLW	301	NNEEAPHEPDGVALVNMKYKKTTPPEYVHCQSAVMSATFAKFHFNLVVGGTYSQIVLW	301	NNEEAPHEPDGVALVNMKYKKTTPPEYVHCQSAVMSATFAKFHFNLVVGGTYSQIVLW
Consensus	271	NNEEAPHEPDGVALVNMKYKKTTPPEYVHCQSAVMSATFAKFHFNLVVGGTYSQIVLW	271	NNEEAPHEPDGVALVNMKYKKTTPPEYVHCQSAVMSATFAKFHFNLVVGGTYSQIVLW	271	NNEEAPHEPDGVALVNMKYKKTTPPEYVHCQSAVMSATFAKFHFNLVVGGTYSQIVLW	271	NNEEAPHEPDGVALVNMKYKKTTPPEYVHCQSAVMSATFAKFHFNLVVGGTYSQIVLW
NP_034194.1 (mouse)	335	DNRSNKRTPVQRTPLSAAAHHPVYCVNVVGTQNAHNLIISTDGGKICSWSLDMLSHPQD	335	DNRSNKRTPVQRTPLSAAAHHPVYCVNVVGTQNAHNLIISTDGGKICSWSLDMLSHPQD	335	DNRSNKRTPVQRTPLSAAAHHPVYCVNVVGTQNAHNLIISTDGGKICSWSLDMLSHPQD	335	DNRSNKRTPVQRTPLSAAAHHPVYCVNVVGTQNAHNLIISTDGGKICSWSLDMLSHPQD
NP_001369.1 (human)	361	DNRSNKRTPVQRTPLSAAAHHPVYCVNVVGTQNAHNLIISTDGGKICSWSLDMLSHPQD	361	DNRSNKRTPVQRTPLSAAAHHPVYCVNVVGTQNAHNLIISTDGGKICSWSLDMLSHPQD	361	DNRSNKRTPVQRTPLSAAAHHPVYCVNVVGTQNAHNLIISTDGGKICSWSLDMLSHPQD	361	DNRSNKRTPVQRTPLSAAAHHPVYCVNVVGTQNAHNLIISTDGGKICSWSLDMLSHPQD
Consensus	330	DNRSNKRTPVQRTPLSAAAHHPVYCVNVVGTQNAHNLIISTDGGKICSWSLDMLSHPQD	330	DNRSNKRTPVQRTPLSAAAHHPVYCVNVVGTQNAHNLIISTDGGKICSWSLDMLSHPQD	330	DNRSNKRTPVQRTPLSAAAHHPVYCVNVVGTQNAHNLIISTDGGKICSWSLDMLSHPQD	330	DNRSNKRTPVQRTPLSAAAHHPVYCVNVVGTQNAHNLIISTDGGKICSWSLDMLSHPQD
NP_034194.1 (mouse)	395	SMELVHKQSKAVAVTSMSPFVGDVNNFVVGSEEGSVYTACRHGSKAGISEMFEGHQGPIT	395	SMELVHKQSKAVAVTSMSPFVGDVNNFVVGSEEGSVYTACRHGSKAGISEMFEGHQGPIT	395	SMELVHKQSKAVAVTSMSPFVGDVNNFVVGSEEGSVYTACRHGSKAGISEMFEGHQGPIT	395	SMELVHKQSKAVAVTSMSPFVGDVNNFVVGSEEGSVYTACRHGSKAGISEMFEGHQGPIT
NP_001369.1 (human)	421	SMELVHKQSKAVAVTSMSPFVGDVNNFVVGSEEGSVYTACRHGSKAGISEMFEGHQGPIT	421	SMELVHKQSKAVAVTSMSPFVGDVNNFVVGSEEGSVYTACRHGSKAGISEMFEGHQGPIT	421	SMELVHKQSKAVAVTSMSPFVGDVNNFVVGSEEGSVYTACRHGSKAGISEMFEGHQGPIT	421	SMELVHKQSKAVAVTSMSPFVGDVNNFVVGSEEGSVYTACRHGSKAGISEMFEGHQGPIT
Consensus	390	SMELVHKQSKAVAVTSMSPFVGDVNNFVVGSEEGSVYTACRHGSKAGISEMFEGHQGPIT	390	SMELVHKQSKAVAVTSMSPFVGDVNNFVVGSEEGSVYTACRHGSKAGISEMFEGHQGPIT	390	SMELVHKQSKAVAVTSMSPFVGDVNNFVVGSEEGSVYTACRHGSKAGISEMFEGHQGPIT	390	SMELVHKQSKAVAVTSMSPFVGDVNNFVVGSEEGSVYTACRHGSKAGISEMFEGHQGPIT
NP_034194.1 (mouse)	455	GIHCHAAVGAVDGSHLFTSSFDWTVKLWTTKNNKPLYSFEDNADYVDVVMWSPTHPALF	455	GIHCHAAVGAVDGSHLFTSSFDWTVKLWTTKNNKPLYSFEDNADYVDVVMWSPTHPALF	455	GIHCHAAVGAVDGSHLFTSSFDWTVKLWTTKNNKPLYSFEDNADYVDVVMWSPTHPALF	455	GIHCHAAVGAVDGSHLFTSSFDWTVKLWTTKNNKPLYSFEDNADYVDVVMWSPTHPALF
NP_001369.1 (human)	481	GIHCHAAVGAVDGSHLFTSSFDWTVKLWTTKNNKPLYSFEDNADYVDVVMWSPTHPALF	481	GIHCHAAVGAVDGSHLFTSSFDWTVKLWTTKNNKPLYSFEDNADYVDVVMWSPTHPALF	481	GIHCHAAVGAVDGSHLFTSSFDWTVKLWTTKNNKPLYSFEDNADYVDVVMWSPTHPALF	481	GIHCHAAVGAVDGSHLFTSSFDWTVKLWTTKNNKPLYSFEDNADYVDVVMWSPTHPALF
Consensus	450	GIHCHAAVGAVDGSHLFTSSFDWTVKLWTTKNNKPLYSFEDNADYVDVVMWSPTHPALF	450	GIHCHAAVGAVDGSHLFTSSFDWTVKLWTTKNNKPLYSFEDNADYVDVVMWSPTHPALF	450	GIHCHAAVGAVDGSHLFTSSFDWTVKLWTTKNNKPLYSFEDNADYVDVVMWSPTHPALF	450	GIHCHAAVGAVDGSHLFTSSFDWTVKLWTTKNNKPLYSFEDNADYVDVVMWSPTHPALF
NP_034194.1 (mouse)	515	ACVDGMGRDLNINNDTEVPTASISVEGNPALNVRVWTHSGREIAVGDSEGGQIVYDVG	515	ACVDGMGRDLNINNDTEVPTASISVEGNPALNVRVWTHSGREIAVGDSEGGQIVYDVG	515	ACVDGMGRDLNINNDTEVPTASISVEGNPALNVRVWTHSGREIAVGDSEGGQIVYDVG	515	ACVDGMGRDLNINNDTEVPTASISVEGNPALNVRVWTHSGREIAVGDSEGGQIVYDVG
NP_001369.1 (human)	541	ACVDGMGRDLNINNDTEVPTASISVEGNPALNVRVWTHSGREIAVGDSEGGQIVYDVG	541	ACVDGMGRDLNINNDTEVPTASISVEGNPALNVRVWTHSGREIAVGDSEGGQIVYDVG	541	ACVDGMGRDLNINNDTEVPTASISVEGNPALNVRVWTHSGREIAVGDSEGGQIVYDVG	541	ACVDGMGRDLNINNDTEVPTASISVEGNPALNVRVWTHSGREIAVGDSEGGQIVYDVG
Consensus	510	ACVDGMGRDLNINNDTEVPTASISVEGNPALNVRVWTHSGREIAVGDSEGGQIVYDVG	510	ACVDGMGRDLNINNDTEVPTASISVEGNPALNVRVWTHSGREIAVGDSEGGQIVYDVG	510	ACVDGMGRDLNINNDTEVPTASISVEGNPALNVRVWTHSGREIAVGDSEGGQIVYDVG	510	ACVDGMGRDLNINNDTEVPTASISVEGNPALNVRVWTHSGREIAVGDSEGGQIVYDVG
NP_034194.1 (mouse)	575	EQIAVPRNDEWARFGRTLAEINANRADAEEEAATRI PA	575	EQIAVPRNDEWARFGRTLAEINANRADAEEEAATRI PA	575	EQIAVPRNDEWARFGRTLAEINANRADAEEEAATRI PA	575	EQIAVPRNDEWARFGRTLAEINANRADAEEEAATRI PA
NP_001369.1 (human)	601	EQIAVPRNDEWARFGRTLAEINANRADAEEEAATRI PA	601	EQIAVPRNDEWARFGRTLAEINANRADAEEEAATRI PA	601	EQIAVPRNDEWARFGRTLAEINANRADAEEEAATRI PA	601	EQIAVPRNDEWARFGRTLAEINANRADAEEEAATRI PA
Consensus	570	EQIAVPRNDEWARFGRTLAEINANRADAEEEAATRI PA	570	EQIAVPRNDEWARFGRTLAEINANRADAEEEAATRI PA	570	EQIAVPRNDEWARFGRTLAEINANRADAEEEAATRI PA	570	EQIAVPRNDEWARFGRTLAEINANRADAEEEAATRI PA

Amino acid identity: 94%
Amino acid similarity: 95%

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Figure 14. Amino Acid Alignment of Mouse, Rattus Norvegicus, and Human Dynein Intermediate Chain 2 Proteins –Highly Conserved Amino Acid Residues.

Software used:

MultAlin via <http://prodes.toulouse.inra.fr/multalin/multalin.html> [Corpet. F. (1988), Multiple sequence alignment with hierarchical clustering, Nucl. Acids Res., 16 (22), 10881-10890]

BOXSHADE 3.21 via http://www.ch.embnet.org/software/BOX_form.html

		1M
NP_034194.1(mouse)	1	MSDKS ¹ ILKAELEKKQRLAQIREKKRKEEERKKKETDQKKEAAVSVQEE ¹ SDLEKKRREA
NP_001369.1(human)	1	MSDKSELKAELEKKQRLAQIREKKRKEEERKKKETDQKKEA ¹ VAPVQEE ¹ SDLEKKRREA
NP_446332.1(rat)	1	MSDKSELKAELEKKQRLAQIREKKRKEEERKKKETDQKKEAAVSVQEE ¹ SDLEKKRREA
Consensus	1	MSDKS ¹ ILKAELEKKQRLAQIREKKRKEEERKKKETDQKKEAAVSVQEE ¹ SDLEKKRREA
NP_034194.1(mouse)	61	EALLQSMGLTTDSPIV ¹PPPMSPSSKSVSTPSEAGSQDSGDGAVGSF ¹
NP_001369.1(human)	61	EALLQSMGLTTDSPIVSEY ¹ WVPPMSPSSKSVSTPSEAGSQDSGDGAVGSRTLHWDTDF ¹
NP_446332.1(rat)	61	EALLQSMGLTTDSPIVSEY ¹ WVPPMSPSSKSVSTPSEAGSQDSGDGAVGSRTLHWDTDF ¹
Consensus	60	EALLQSMGLTTDSPIVSEY ¹ WVPPMSPSSKSVSTPSEAGSQDSGDGAVGSRTLHWDTDF ¹
		148F 149P 155T 165M
NP_034194.1(mouse)	107SGPIKLGMAKITQVDFPPREIVTYTKETQTPVTAQPKDEEEEDDVAT ¹
NP_001369.1(human)	121	SVLQLHSDSDLCGRGPIKLGMAKITQVDFPPREIVTYTKETQTPVTAQPKDEEEEDDVAA ¹
NP_446332.1(rat)	121	SVLQLHSDSDLCGRGPIKLGMAKITQVDFPPREIVTYTKETQTPVTAQPKDEEEEDDVAA ¹
Consensus	118	S.LQLHSDSDLCGRGPIKLGMAKITQVDFPPREIVTYTKETQTPVTAQPKDEEEEDDVAA ¹
NP_034194.1(mouse)	155	PKPPVEPEEEKTLKKDEENDSKAPPHELTEEEKQIILHSEEF ¹ LSFFDHSTRIVERALSEQ ¹
NP_001369.1(human)	181	PKPPVEPEEEKTLKKDEENDSKAPPHELTEEEKQIILHSEEF ¹ LSFFDHSTRIVERALSEQ ¹
NP_446332.1(rat)	181	PKPPVEPEEEKTLKKDEENDSKAPPHELTEEEKQIILHSEEF ¹ LSFFDHSTRIVERALSEQ ¹
Consensus	176	PKPPVEPEEEKTLKKDEENDSKAPPHELTEEEKQIILHSEEF ¹ LSFFDHSTRIVERALSEQ ¹
		252L
NP_034194.1(mouse)	215	INIFFDYSGRDLEDKEGEIQAGAKLSLNROFFDERWSKHRVVSCLDWSSQYPELLVASYN ¹
NP_001369.1(human)	241	INIFFDYSGRDLEDKEGEIQAGAKLSLNROFFDERWSKHRVVSCLDWSSQYPELLVASYN ¹
NP_446332.1(rat)	241	INIFFDYSGRDLEDKEGEIQAGAKLSLNROFFDERWSKHRVVSCLDWSSQYPELLVASYN ¹
Consensus	235	INIFFDYSGRDLEDKEGEIQAGAKLSLNROFFDERWSKHRVVSCLDWSSQYPELLVASYN ¹
		323T
NP_034194.1(mouse)	275	NNEEAPHEPDGVALVNNMKYKKTTPYVVFHCQSAVMSATFAK ¹ FHPNLVVG ¹ GYSGQIVLW ¹
NP_001369.1(human)	301	NNEEAPHEPDGVALVNNMKYKKTTPYVVFHCQSAVMSATFAK ¹ FHPNLVVG ¹ GYSGQIVLW ¹
NP_446332.1(rat)	301	NNEEAPHEPDGVALVNNMKYKKTTPYVVFHCQSAVMSATFAK ¹ FHPNLVVG ¹ GYSGQIVLW ¹
Consensus	295	NNEEAPHEPDGVALVNNMKYKKTTPYVVFHCQSAVMSATFAK ¹ FHPNLVVG ¹ GYSGQIVLW ¹
NP_034194.1(mouse)	335	DNRSNKRTPVQRTPLSAAAH ¹ THEPVYCVNVVGTQNAHNLISISTD ¹ GKICSWSLDMLSH ¹ PQD ¹
NP_001369.1(human)	361	DNRSNKRTPVQRTPLSAAAH ¹ THEPVYCVNVVGTQNAHNLISISTD ¹ GKICSWSLDMLSH ¹ PQD ¹
NP_446332.1(rat)	361	DNRSNKRTPVQRTPLSAAAH ¹ THEPVYCVNVVGTQNAHNLISISTD ¹ GKICSWSLDMLSH ¹ PQD ¹
Consensus	354	DNRSNKRTPVQRTPLSAAAH ¹ THEPVYCVNVVGTQNAHNLISISTD ¹ GKICSWSLDMLSH ¹ PQD ¹
NP_034194.1(mouse)	395	SMELVHKQSKAVAVTSMSPFVGDVNNFVVGSEEGSVYTACRHGSKAGISEMFE ¹ GHQGPIT ¹
NP_001369.1(human)	421	SMELVHKQSKAVAVTSMSPFVGDVNNFVVGSEEGSVYTACRHGSKAGISEMFE ¹ GHQGPIT ¹
NP_446332.1(rat)	421	SMELVHKQSKAVAVTSMSPFVGDVNNFVVGSEEGSVYTACRHGSKAGISEMFE ¹ GHQGPIT ¹
Consensus	414	SMELVHKQSKAVAVTSMSPFVGDVNNFVVGSEEGSVYTACRHGSKAGISEMFE ¹ GHQGPIT ¹
NP_034194.1(mouse)	455	GIHCHAAVGA ¹ VD ¹ FSHLFVTS ¹ FDWTVKLWTTKNNKPLYSFEDNSDYVYDV ¹ VMWSPTH ¹ PALF ¹
NP_001369.1(human)	481	GIHCHAAVGA ¹ VD ¹ FSHLFVTS ¹ FDWTVKLWTTKNNKPLYSFEDNSDYVYDV ¹ VMWSPTH ¹ PALF ¹
NP_446332.1(rat)	481	GIHCHAAVGA ¹ VD ¹ FSHLFVTS ¹ FDWTVKLWTTKNNKPLYSFEDNSDYVYDV ¹ VMWSPTH ¹ PALF ¹
Consensus	474	GIHCHAAVGA ¹ VD ¹ FSHLFVTS ¹ FDWTVKLWTTKNNKPLYSFEDNSDYVYDV ¹ VMWSPTH ¹ PALF ¹
NP_034194.1(mouse)	515	ACVDGMGRDLNLNNDTEVPTASISVEGNPALNRVRWTHSGREIAVGDS ¹ EGQIVYIDVG ¹
NP_001369.1(human)	541	ACVDGMGRDLNLNNDTEVPTASISVEGNPALNRVRWTHSGREIAVGDS ¹ EGQIVYIDVG ¹
NP_446332.1(rat)	541	ACVDGMGRDLNLNNDTEVPTASISVEGNPALNRVRWTHSGREIAVGDS ¹ EGQIVYIDVG ¹
Consensus	534	ACVDGMGRDLNLNNDTEVPTASISVEGNPALNRVRWTHSGREIAVGDS ¹ EGQIVYIDVG ¹

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(Figure 13 continued)

NP_034194.1 (mouse)	575	EQIAVPRNDEWARFGRTLAEINANRADAEEEEATRIP
NP_001369.1 (human)	601	EQIAVPRNDEWARFGRTLAEINANRADAEEEEATRIP
NP_446332.1 (rat)	601	EQIAVPRNDEWARFGRTLAEINANRADAEEEEATRIP
Consensus	594	EQIAVPRNDEWARFGRTLAEINANRADAEEEEATRIP

Amino acid identity: 93,5%

Amino acid similarity: 94,5%

The following binding domains are indicated (positions correspond to the human amino acid sequence):

P150d (DCTN1 (p150) binding domain)	1M-149P
Tctex1d (Tctex1 binding domain)	148F-165T
10kDa (10kda light chain binding domain)	155T-165T
2Bd (2B light chain binding domain)	252L-323T

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Figure 15. Amino Acid Alignment of Mouse and Human DCTN1 (p150) Proteins – highly conserved Amino Acid Residues.

Software used:

- MultAlin via <http://prodes.toulouse.inra.fr/multalin/multalin.html> [Corpet. F. (1988), Multiple sequence alignment with hierarchical clustering, Nucl. Acids Res., 16 (22), 10881-10890]

- BOXSHADE 3.21 via http://www.ch.embnet.org/software/BOX_form.html

NP_031861.1(mouse)	1	MAQSRHRHSSRTPSGSRMS	TEASARPLRVGSRVEVIGKGRGTVAIVGATLFATGKWWGV
AAD55811.1(human)	1	MAQSRHRHYSRTPSGSRMSAEASARPLRVGSRVEVIGKGRGTVAIVGATLFATGKWWGV	
Consensus	1	MAQSRHRHSSRTPSGSRMSAEASARPLRVGSRVEVIGKGRGTVAIVGATLFATGKWWGV	
NP_031861.1(mouse)	61	ILDEAKGKNDGTVOGPKYFTCDEGHGIFVRQSQIQVFEDGADTTSPETPDSSASKVLKRE	
AAD55811.1(human)	61	ILDEAKGKNDGTVOGPKYFTCDEGHGIFVRQSQIQVFEDGADTTSPETPDSSASKVLKRE	
Consensus	61	ILDEAKGKNDGTVOGPKYFTCDEGHGIFVRQSQIQVFEDGADTTSPETPDSSASKVLKRE	
NP_031861.1(mouse)	121	GADAAAKTSKLRGLKPKFAPTARKTTTRRPKPTRPASTGVAG	ESSSLGPSGSASAGELSS
AAD55811.1(human)	121	GADTTAKTSKLRGLKPKFAPTARKTTTRRPKPTRPASTGVAGASSSLGPSGSASAGELSS	
Consensus	121	GADAAAKTSKLRGLKPKFAPTARKTTTRRPKPTRPASTGVAGASSSLGPSGSASAGELSS	
NP_031861.1(mouse)	181	SEPSTPAQTPLAAPIIPTPALTSPGAAPPLPSPSKEEEGLRAQVRDLEEKLETIRLKRSE	
AAD55811.1(human)	181	SEPSTPAQTPLAAPIIPTPALTSPGAAPPLPSPSKEEEGLRAQVRDLEEKLETIRLKRSE	
Consensus	181	SEPSTPAQTPLAAPIIPTPALTSPGAAPPLPSPSKEEEGLRAQVRDLEEKLETIRLKRSE	
NP_031861.1(mouse)	241	DKAKLKELEKHKIQLEQVQEWKSKMQEQQADLQRLKEARKEAKEALEAKERYNEEMADT	
AAD55811.1(human)	241	DKAKLKELEKHKIQLEQVQEWKSKMQEQQADLQRLKEARKEAKEALEAKERYNEEMADT	
Consensus	241	DKAKLKELEKHKIQLEQVQEWKSKMQEQQADLQRLKEARKEAKEALEAKERYNEEMADT	
NP_031861.1(mouse)	301	ADAIEMATLDKEMAEERAESLQOEVEALKERVDELTTDLEILKAEIEEKSGDGAASSYQL	
AAD55811.1(human)	301	ADAIEMATLDKEMAEERAESLQOEVEALKERVDELTTDLEILKAEIEEKSGDGAASSYQL	
Consensus	301	ADAIEMATLDKEMAEERAESLQOEVEALKERVDELTTDLEILKAEIEEKSGDGAASSYQL	
NP_031861.1(mouse)	361	KQLEEQNARLKDALVPMRDLSSSEKQEHVKLQKLMKKNQLEVVRRQERLQEELSQAE	
AAD55811.1(human)	361	KQLEEQNARLKDALVPMRDLSSSEKQEHVKLQKLMKKNQLEVVRRQERLQEELSQAE	
Consensus	361	KQLEEQNARLKDALVPMRDLSSSEKQEHVKLQKLMKKNQLEVVRRQERLQEELSQAE	
NP_031861.1(mouse)	421	STIDELKEQVDAALGAEENVEMLTDRNLNLEEKVRELRETVDLEAMNEMNDLQENARE	
AAD55811.1(human)	421	STIDELKEQVDAALGAEENVEMLTDRNLNLEEKVRELRETVDLEAMNEMNDLQENARE	
Consensus	421	STIDELKEQVDAALGAEENVEMLTDRNLNLEEKVRELRETVDLEAMNEMNDLQENARE	
NP_031861.1(mouse)	481	TELELREQLDNAGARVREAAQKRVAAQETVADYQQTIKKYRQLTAHLQDVNRELTNQOE	
AAD55811.1(human)	481	TELELREQLDNAGARVREAAQKRVAAQETVADYQQTIKKYRQLTAHLQDVNRELTNQOE	
Consensus	481	TELELREQLDNAGARVREAAQKRVAAQETVADYQQTIKKYRQLTAHLQDVNRELTNQOE	
NP_031861.1(mouse)	541	SVERQQQPPPETFDFFIKFAETKAHAKAIEMLRQMEVAQANRHMSLLTAFMPDSEFLRPG	
AAD55811.1(human)	541	SVERQQQPPPETFDFFIKFAETKAHAKAIEMLRQMEVAQANRHMSLLTAFMPDSEFLRPG	
Consensus	541	SVERQQQPPPETFDFFIKFAETKAHAKAIEMLRQMEVAQANRHMSLLTAFMPDSEFLRPG	
NP_031861.1(mouse)	601	GDHDCVLVLLMPRLICFAELIRKQAQEKFLSENCSERPGLRGAAQEQLSFAAGLVYSI	
AAD55811.1(human)	601	GDHDCVLVLLMPRLICFAELIRKQAQEKFLSENCSERPGLRGAAQEQLSFAAGLVYSI	
Consensus	601	GDHDCVLVLLMPRLICFAELIRKQAQEKFLSENCSERPGLRGAAQEQLSFAAGLVYSI	
NP_031861.1(mouse)	661	SLIQATLHRYEHALSQCSVDVYKVGSLYPMSAHERSLDFLIELLHKDQDDETNNVEPL	
AAD55811.1(human)	661	SLIQATLHRYEHALSQCSVDVYKVGSLYPMSAHERSLDFLIELLHKDQDDETNNVEPL	
Consensus	660	SLIQATLHRYEHALSQCSVDVYKVGSLYPMSAHERSLDFLIELLHKDQDDETNNVEPL	
NP_031861.1(mouse)	721	NKAIKYYQHLYRIHLAEQPEDCTMQLADHIKFTQSALDCMGVEVGRRLRAFLQGGQEATDI	
AAD55811.1(human)	721	NKAIKYYQHLYRIHLAEQPEDCTMQLADHIKFTQSALDCMGVEVGRRLRAFLQGGQEATDI	
Consensus	720	NKAIKYYQHLYRIHLAEQPEDCTMQLADHIKFTQSALDCMGVEVGRRLRAFLQGGQEATDI	

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(Figure 15 continued)

NP_031861.1 (mouse)	781	ALLLRDLETSCSDIRQFCCKIRRRMPGTDAPGIPAALAFGSQVSDTLDDCRKHLTWVVAV
AAD55811.1 (human)	781	ALLLRDLETSCSDIRQFCCKIRRRMPGTDAPGIPAALAFGQVSDTLDDCRKHLTWVVAV
Consensus	780	ALLLRDLETSCSDIRQFCCKIRRRMPGTDAPGIPAALAFGQVSDTLDDCRKHLTWVVAV
NP_031861.1 (mouse)	841	LQEVAAAAQLIAPLAENEGLVAALEELAFKASEQIYGSPSSSPYECLRQSCNIIISTM
AAD55811.1 (human)	841	LQEVAAAAQLIAPLAENEGLVAALEELAFKASEQIYGSPSSSPYECLRQSCNIIISTM
Consensus	840	LQEVAAAAQLIAPLAENEGLVAALEELAFKASEQIYGSPSSSPYECLRQSCNIIISTM
NP_031861.1 (mouse)	901	NKLATAMQEGEYDAERPPSKPPVELRAALRAEITDAEGLGLKLEDRETVIKELKSLK
AAD55811.1 (human)	901	NKLATAMQEGEYDAERPPSKPPVELRAALRAEITDAEGLGLKLEDRETVIKELKSLK
Consensus	900	NKLATAMQEGEYDAERPPSKPPVELRAALRAEITDAEGLGLKLEDRETVIKELKSLK
NP_031861.1 (mouse)	961	IKGEELSEANVRLSLEKKLDSAAKDADERIEKVQTRLDETQALLRKKENFEETMDALC
AAD55811.1 (human)	961	IKGEELSEANVRLSLEKKLDSAAKDADERIEKVQTRLDETQALLRKKENFEETMDALC
Consensus	960	IKGEELSEANVRLSLEKKLDSAAKDADERIEKVQTRLDETQALLRKKENFEETMDALC
NP_031861.1 (mouse)	1021	ADIDQLEAEKAEKQRLNSQSKRTIEGLRGPSPGIATLVSGIAGEEQRGAPGQAPGA
AAD55811.1 (human)	1021	ADIDQLEAEKAEKQRLNSQSKRTIEGLRGPSPGIATLVSGIAGEEQRGAPGQAPGA
Consensus	1018	ADIDQLEAEKAEKQRLNSQSKRTIEGLRGPSPGIATLVSGIAGEEQRGAPGQAPGA
NP_031861.1 (mouse)	1081	LPGPGLVKDSPLLLQQISAMRLHISQLOHENSILRGAQMKSALALPPLHVAKLSLPPHE
AAD55811.1 (human)	1081	LPGPGLVKDSPLLLQQISAMRLHISQLOHENSILRGAQMKSALALPPLHVAKLSLPPHE
Consensus	1078	LPGPGLVKDSPLLLQQISAMRLHISQLOHENSILRGAQMKSALALPPLHVAKLSLPPHE
NP_031861.1 (mouse)	1141	GPGGNLVAGALYRKTSQLEKLNQLSTHTHVVDITRSSPAAKSFSQALMEQVAQLKSLSD
AAD55811.1 (human)	1138	GPGSELVAGALYRKTSQLEKLNQLSTHTHVVDITRSSPAAKSFSQALMEQVAQLKSLSD
Consensus	1135	GPGGNLVAGALYRKTSQLEKLNQLSTHTHVVDITRSSPAAKSFSQALMEQVAQLKSLSD
NP_031861.1 (mouse)	1201	TEKLDKDEVLKETVQRPGATVPTDFATFPSSAFLRAKEEQDDTVYMGKVTFSCAAGLG
AAD55811.1 (human)	1198	TEKLDKDEVLKETVQRPGATVPTDFATFPSSAFLRAKEEQDDTVYMGKVTFSCAAGLG
Consensus	1194	TEKLDKDEVLKETVQRPGATVPTDFATFPSSAFLRAKEEQDDTVYMGKVTFSCAAGLG
NP_031861.1 (mouse)	1261	QRHRLVLTQEQLHQLHSRLIS
AAD55811.1 (human)	1258	QRHRLVLTQEQLHQLHSRLIS
Consensus	1253	QRHRLVLTQEQLHQLHSRLIS

Amino acid identity 97%
Amino acid similarity 98%

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Figure 16. Amino Acid Alignment of Mouse, Rattus Norvegicus, and Human DCTN1 (p150) Proteins – highly conserved Amino Acid Residues.

Software used:

- MultAlin via <http://prodes.toulouse.inra.fr/multalin/multalin.html> [Corpet. F. (1988), Multiple sequence alignment with hierarchical clustering, Nucl. Acids Res., 16 (22), 10881-10890]

- BOXSHADE 3.21 via http://www.ch.embnet.org/software/BOX_form.html

		39G	
NP_031861.1 (mouse)	1	MAQSRHMS	SRTPSGSRMSTEASARPLRVGS
NP_077044.1 (rat)	1	MAQSKRHM	YRTPSGSRMSTEASARPLRVGS
AAD55811.1 (human)	1	MAQSKRHM	YSRTPSGSRMS
Consensus	1	MAQSKRHM	YSRTPSGSRMSTEASARPLRVGS
		133G 150P	
NP_031861.1	61	ILDEAKGKNDGT	VQGRKFTFCDEGHGIFVRQSQIQVFEDGADTTSPETPDSSASKVLKRE
NP_077044.1	61	ILDEAKGKNDGT	VQGRKFTFCDEGHGIFVRQSQIQVFEDGADTTSPETPDSSASKVLKRE
AAD55811.1	61	ILDEAKGKNDGT	VQGRKFTFCDEGHGIFVRQSQIQVFEDGADTTSPETPDSSASKVLKRE
Consensus	61	ILDEAKGKNDGT	VQGRKFTFCDEGHGIFVRQSQIQVFEDGADTTSPETPDSSASKVLKRE
NP_031861.1	121	GADAAAKTSKLRGL	KPKAFTARKTTTRRFPKTRPASTGVAGPSSSLGPSGSASAGELSS
NP_077044.1	121	GADAAAKTSKLRGL	KPKAFTARKTTTRRFPKTRPASTGVAGPSSSLGPSGSASAGELSS
AAD55811.1	121	GADAAAKTSKLRGL	KPKAFTARKTTTRRFPKTRPASTGVAGPSSSLGPSGSASAGELSS
Consensus	120	GADAAAKTSKLRGL	KPKAFTARKTTTRRFPKTRPASTGVAGPSSSLGPSGSASAGELSS
NP_031861.1	181	SEPSTPAQTPLA	APIIPTPALTSPGAAPPLPSPSKEEEGLRAQVRDLEEKLETLRKRSE
NP_077044.1	181	SEPSTPAQTPLA	APIIPTPALTSPGAAPPLPSPSKEEEGLRAQVRDLEEKLETLRKRSE
AAD55811.1	181	SEPSTPAQTPLA	APIIPTPALTSPGAAPPLPSPSKEEEGLRAQVRDLEEKLETLRKRSE
Consensus	180	SEPSTPAQTPLA	APIIPTPALTSPGAAPPLPSPSKEEEGLRAQVRDLEEKLETLRKRSE
NP_031861.1	241	DKAKLKELEKHKI	QLEQVQEWKSKMQEQADLQRLKEARKEAKEALEAKERYMEEMADT
NP_077044.1	241	DKAKLKELEKHKI	QLEQVQEWKSKMQEQADLQRLKEARKEAKEALEAKERYMEEMADT
AAD55811.1	241	DKAKLKELEKHKI	QLEQVQEWKSKMQEQADLQRLKEARKEAKEALEAKERYMEEMADT
Consensus	240	DKAKLKELEKHKI	QLEQVQEWKSKMQEQADLQRLKEARKEAKEALEAKERYMEEMADT
NP_031861.1	301	ADAIEMATLDK	MAEERAEESLQQEVEALKERVDELTTDLEILKAEIEEKSGDGAASSYQL
NP_077044.1	300	ADAIEMATLDK	MAEERAEESLQQEVEALKERVDELTTDLEILKAEIEEKSGDGAASSYQL
AAD55811.1	301	ADAIEMATLDK	MAEERAEESLQQEVEALKERVDELTTDLEILKAEIEEKSGDGAASSYQL
Consensus	300	ADAIEMATLDK	MAEERAEESLQQEVEALKERVDELTTDLEILKAEIEEKSGDGAASSYQL
NP_031861.1	361	KQLEEQNARLKD	ALVNRDLSSSEKQEHVKLQKLMEKNQLELVVRQQRERLQEELSQA
NP_077044.1	360	KQLEEQNARLKD	ALVNRDLSSSEKQEHVKLQKLMEKNQLELVVRQQRERLQEELSQA
AAD55811.1	361	KQLEEQNARLKD	ALVNRDLSSSEKQEHVKLQKLMEKNQLELVVRQQRERLQEELSQA
Consensus	360	KQLEEQNARLKD	ALVNRDLSSSEKQEHVKLQKLMEKNQLELVVRQQRERLQEELSQA
NP_031861.1	421	STIDELKEQVDA	ALGAEENVEMLTDRNLNLEEKVRELFEETVGDLEAMNEMNDELQENARE
NP_077044.1	420	STIDELKEQVDA	ALGAEENVEMLTDRNLNLEEKVRELFEETVGDLEAMNEMNDELQENARE
AAD55811.1	421	STIDELKEQVDA	ALGAEENVEMLTDRNLNLEEKVRELFEETVGDLEAMNEMNDELQENARE
Consensus	420	STIDELKEQVDA	ALGAEENVEMLTDRNLNLEEKVRELFEETVGDLEAMNEMNDELQENARE
NP_031861.1	481	TELELREQLDM	AGARVFEAQRVEAAQETVADYQQTIKKYRQLTAHLQDVNRELTNQQA
NP_077044.1	480	TELELREQLDM	AGARVFEAQRVEAAQETVADYQQTIKKYRQLTAHLQDVNRELTNQQA
AAD55811.1	481	TELELREQLDM	AGARVFEAQRVEAAQETVADYQQTIKKYRQLTAHLQDVNRELTNQQA
Consensus	480	TELELREQLDM	AGARVFEAQRVEAAQETVADYQQTIKKYRQLTAHLQDVNRELTNQQA
NP_031861.1	541	SVERQQQPPPET	FDYIKFAETKAHAKAIEMLRQMEVAQANRHMSLLTAFMPDSFLRPG
NP_077044.1	540	SVERQQQPPPET	FDYIKFAETKAHAKAIEMLRQMEVAQANRHMSLLTAFMPDSFLRPG
AAD55811.1	541	SVERQQQPPPET	FDYIKFAETKAHAKAIEMLRQMEVAQANRHMSLLTAFMPDSFLRPG
Consensus	540	SVERQQQPPPET	FDYIKFAETKAHAKAIEMLRQMEVAQANRHMSLLTAFMPDSFLRPG
NP_031861.1	601	GDHDCVLVLLM	PRICKAELIRKQAEKFDLSENCSERPGLRGAAGEQLSFAAGLVYSI
NP_077044.1	600	GDHDCVLVLLM	PRICKAELIRKQAEKFDLSENCSERPGLRGAAGEQLSFAAGLVYSI
AAD55811.1	601	GDHDCVLVLLM	PRICKAELIRKQAEKFDLSENCSERPGLRGAAGEQLSFAAGLVYSI
Consensus	600	GDHDCVLVLLM	PRICKAELIRKQAEKFDLSENCSERPGLRGAAGEQLSFAAGLVYSI

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(Figure 16 continued)

NP_031861.1	661	SLLOATLHRYEHALSQCSVDVYKKVGSYPMSAHERSLDFLIELLHKDQDDETNNVEPL
NP_077044.1	660	SLLOATLHRYEHALSQCSVDVYKKVGSYPMSAHERSLDFLIELLHKDQDDETNNVEPL
AAD55811.1	661	SLLOATLHRYEHALSQCSVDVYKKVGSYPMSAHERSLDFLIELLHKDQDDETNNVEPL
Consensus	659	SLLOATLHRYEHALSQCSVDVYKKVGSYPMSAHERSLDFLIELLHKDQDDETNNVEPL
NP_031861.1	721	NKGIKYQHLYSIHLEQPEDSTMQLADHIKFTQSALDCMSVEVGRLEAFLOGGQEQATDI
NP_077044.1	720	TKAIKYQHLYSIHLEQPEDSTMQLADHIKFTQSALDCMSVEVGRLEAFLOGGQEQATDI
AAD55811.1 (human)	721	TKAIKYQHLYSIHLEQPEDSTMQLADHIKFTQSALDCMSVEVGRLEAFLOGGQEQATDI
Consensus	719	TKAIKYQHLYSIHLEQPEDSTMQLADHIKFTQSALDCMSVEVGRLEAFLOGGQEQATDI
NP_031861.1	781	ALLLRDLETSCSDIRQFCKKIRRRMPGTDAPGIPAAALAFGSQVSDTLDCRKHHTWVVAV
NP_077044.1	780	ALLLRDLETSCSDIRQFCKKIRRRMPGTDAPGIPAAALAFGSQVSDTLDCRKHHTWVVAV
AAD55811.1 (human)	781	ALLLRDLETSCSDIRQFCKKIRRRMPGTDAPGIPAAALAFGSQVSDTLDCRKHHTWVVAV
Consensus	778	ALLLRDLETSCSDIRQFCKKIRRRMPGTDAPGIPAAALAFGSQVSDTLDCRKHHTWVVAV
NP_031861.1	841	LQEVAAAAQLIAPLAENEGLPVAALEELAFKASEQIYGSPPSSPYECLRQSCNIIILISTM
NP_077044.1	840	LQEVAAAAQLIAPLAENEGLPVAALEELAFKASEQIYGSPPSSPYECLRQSCNIIILISTM
AAD55811.1 (human)	841	LQEVAAAAQLIAPLAENEGLPVAALEELAFKASEQIYGSPPSSPYECLRQSCNIIILISTM
Consensus	838	LQEVAAAAQLIAPLAENEGLPVAALEELAFKASEQIYGSPPSSPYECLRQSCNIIILISTM
NP_031861.1	901	NKLATAMQEGEYDAERPPSKPPVVELRAAALRAEITDAEGLGLKLEDRETIVIKELKKSLE
NP_077044.1	900	NKLATAMQEGEYDAERPPSKPPVVELRAAALRAEITDAEGLGLKLEDRETIVIKELKKSLE
AAD55811.1 (human)	901	NKLATAMQEGEYDAERPPSKPPVVELRAAALRAEITDAEGLGLKLEDRETIVIKELKKSLE
Consensus	897	NKLATAMQEGEYDAERPPSKPPVVELRAAALRAEITDAEGLGLKLEDRETIVIKELKKSLE
NP_031861.1	961	IKGEELSEANVRLSLLEKKLDSAADADDERIEKVQTRLTETQTLRKKEKEFEETMDALQ
NP_077044.1	960	IKGEELSEANVRLSLLEKKLDSAADADDERIEKVQTRLTETQTLRKKEKEFEETMDALQ
AAD55811.1 (human)	961	IKGEELSEANVRLSLLEKKLDSAADADDERIEKVQTRLTETQTLRKKEKEFEETMDALQ
Consensus	957	IKGEELSEANVRLSLLEKKLDSAADADDERIEKVQTRLTETQTLRKKEKEFEETMDALQ
NP_031861.1	1021	ADIDQLEAEKAEKRLNSQSKRTIEGLRGPSPGIATLVSGIAGEEQQRGGAPGAPGA
NP_077044.1	1020	ADIDQLEAEKAEKRLNSQSKRTIEGLRGPSPGIATLVSGIAGEEQQRGGAPGAPGA
AAD55811.1 (human)	1021	ADIDQLEAEKAEKRLNSQSKRTIEGLRGPSPGIATLVSGIAGEEQQRGGAPGAPGA
Consensus	1015	ADIDQLEAEKAEKRLNSQSKRTIEGLRGPSPGIATLVSGIAGEEQQRGGAPGAPGA
NP_031861.1	1081	LPGPGLVKDSPLLQQISAMRLHISQLQHENSILRGAQMKASLAALPPLHVAKLSLPPHE
NP_077044.1	1080	LPGPGLVKDSPLLQQISAMRLHISQLQHENSILRGAQMKASLAALPPLHVAKLSLPPHE
AAD55811.1 (human)	1081	LPGPGLVKDSPLLQQISAMRLHISQLQHENSILRGAQMKASLAALPPLHVAKLSLPPHE
Consensus	1074	LPGPGLVKDSPLLQQISAMRLHISQLQHENSILRGAQMKASLAALPPLHVAKLSLPPHE
NP_031861.1	1141	GPGGNLSGALYRKTSQLEKLNQLSTHTHVVDITRSPAAKSPSAQLMEQVAQLKSLSD
NP_077044.1	1140	GPGGNLSGALYRKTSQLEKLNQLSTHTHVVDITRSPAAKSPSAQLMEQVAQLKSLSD
AAD55811.1 (human)	1138	GPGGNLSGALYRKTSQLEKLNQLSTHTHVVDITRSPAAKSPSAQLMEQVAQLKSLSD
Consensus	1134	GPGGNLSGALYRKTSQLEKLNQLSTHTHVVDITRSPAAKSPSAQLMEQVAQLKSLSD
NP_031861.1	1201	PIEKLKDEVLEKETVTQRPATVPTDFATFPSSAFLRAKEEQDDTVYMGKVTFSCAAGLG
NP_077044.1	1200	PIEKLKDEVLEKETVTQRPATVPTDFATFPSSAFLRAKEEQDDTVYMGKVTFSCAAGLG
AAD55811.1 (human)	1198	PIEKLKDEVLEKETVTQRPATVPTDFATFPSSAFLRAKEEQDDTVYMGKVTFSCAAGLG
Consensus	1192	PIEKLKDEVLEKETVTQRPATVPTDFATFPSSAFLRAKEEQDDTVYMGKVTFSCAAGLG
NP_031861.1	1261	QRHRLVLTQEQHLHQLHSRLIS
NP_077044.1	1260	QRHRLVLTQEQHLHQLHSRLIS
AAD55811.1 (human)	1258	QRHRLVLTQEQHLHQLHSRLIS
Consensus	1251	QRHRLVLTQEQHLHQLHSRLIS

Amino acid identity: 95%

Amino acid similarity: 96%

The following binding domains are indicated by their N-terminal and C-terminal amino acid (positions correspond to the human amino acid sequence):

Microd (microtubules binding domain)	39G – 150P
Dict (dynein intermediate chain1 binding domain)	133G-899T
ARP1d (ARP1 binding domain)	1006R-1021A

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